

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:35 : Search time 14.2364 Seconds  
(without alignments)  
1276.267 Million cell updates/sec

Title: US-09-658-699-2  
Perfect score: 1004  
Sequence: 1 MLGSRVWLMLLLPPTAQR.....QAFVAVARVFAHGAATLSP 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	10.0	204	1 FQHUGL	granulocyte colony
2	99.5	9.9	194	2 T09255	granulocyte colony
3	91	9.1	208	1 S29549	interleukin-6 - sh
4	90.5	9.0	174	2 T10268	granulocyte colony
5	88.5	8.8	207	2 A24573	granulocyte colony
6	87.5	8.7	208	2 A26496	granulocyte colony
7	86	8.6	1121	2 A82809	exodeoxyribonuclea
8	85	8.5	211	1 TCM586	interleukin-6 prec
9	80.5	8.0	232	2 D70537	hypothetical prote
10	80.5	8.0	530	2 D96810	hypothetical prote
11	80	8.0	858	2 JC7683	taste receptor T1R
12	79.5	7.9	201	2 A42247	myelomonocytic gro
13	79	7.9	506	2 AG0893	aerotoxis receptor
14	79	7.9	2512	1 XYCHFA	enoyl-lacyl-carrie
15	78	7.8	1026	2 T05882	hypothetical prote
16	77.5	7.7	513	2 C82366	conserved hypothet
17	77.5	7.7	967	2 G86229	hypothetical prote
18	76.5	7.6	399	2 A11929	N-acetyl-glucosami
19	76.5	7.6	881	2 F84404	valyl-trna synthet
20	76	7.6	262	2 A84240	molybdopterin oxid
21	75.5	7.5	214	2 JC5043	granulocyte colony
22	75.5	7.5	265	2 B83395	probable enoyl-CoA
23	75.5	7.5	938	2 A56731	chromatin assembly
24	75.5	7.5	2304	2 T07920	probable acetyl-Co
25	75	7.5	195	2 I47070	interferon omega -
26	75	7.5	211	2 A34247	interleukin-6 prec
27	75	7.5	801	1 S00943	glucose dehydrogen
28	75	7.5	975	2 T48107	hypothetical prote
29	74.5	7.4	212	2 I46621	pinterleukin 6 -

30	74.5	7.4	212	2 I46590	interleukin 6 - pi
31	74.5	7.4	280	2 S75845	hypothetical prote
32	74	7.4	314	2 T27137	hypothetical prote
33	74	7.4	374	2 T26739	hypothetical prote
34	74	7.4	974	2 A86263	F13K23.18 protein
35	74	7.4	1148	2 AD0198	transcription-tepa
36	73.5	7.3	247	2 H70916	probable glucose-6
37	73.5	7.3	310	2 B90696	probable glutamina
38	73.5	7.3	310	2 F85546	probable glutamina
39	73.5	7.3	649	2 T04005	probable protein k
40	73.5	7.3	755	2 D75598	photoreceptor - De
41	73.5	7.3	1015	2 I39697	beta-galactosidase
42	73	7.3	346	2 A58583	testosterone-resis
43	73	7.3	462	2 AI2319	UDP-N-acetylmuramo
44	72.5	7.2	259	2 T28147	class II histocomp
45	72.5	7.2	374	2 C98215	oligopeptide ABC t

ALIGNMENTS

RESULT 1  
FQHUGL  
granulocyte colony-stimulating factor precursor - human  
N:Alternate names: colony-stimulating factor 3; G-CSF  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1988 #sequence\_revision 18-Aug-1995 #text\_change 22-Jun-1999  
C:Accession: A25093; A49796; A47587; S68331  
R:Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M  
EMBO J. 5, 575-581, 1986  
A:Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-st  
A:Reference number: A25093; MUID:86220137; PMID:2423327  
A:Accession: A25093  
A:Molecule type: DNA; mRNA  
A:Residues: 1-204 <NAG>  
A:Cross-references: EMBL:X03656; EMBL:X03655; NID:X31693; PIDN:CAA35882.1; PID:g73276  
R:Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.  
J. Leukoc. Biol. 41, 302-306, 1987  
A:Title: Expression of granulocyte colony-stimulating factor by human cell lines.  
A:Reference number: A49796; MUID:87196936; PMID:3494801  
A:Accession: A49796  
A:Molecule type: mRNA  
A:Residues: 1-204 <DEV>  
A:Cross-references: GB:M17706; NID:g183040; PIDN:AAA35882.1; PID:g183041  
R:Souza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Muddock, D.C.; Cha  
Science 232, 61-65, 1986  
A:Title: Recombinant human granulocyte colony-stimulating factor: effects  
A:Reference number: A47587; MUID:86151684; PMID:2420009  
A:Accession: A47587  
A:Molecule type: mRNA  
A:Residues: 19-204 <SOU>  
A:Cross-references: GB:M13008; NID:g183044; PIDN:AAA03056.1; PID:g183045  
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.  
Arch. Biochem. Biophys. 324, 344-356, 1995  
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.  
A:Reference number: S68331; MUID:96132662; PMID:8554326  
A:Accession: S68331  
A:Molecule type: protein  
A:Residues: 1-31-46 <HAN>  
C:Genetics:  
A:Gene: GDB:CSF3  
A:Cross-references: GDB:I19083; OMIM:138970  
A:Map position: 17q11.2-17q12  
A:Introns: 14/1; 65/3; 101/3; 150/3  
C:Function:  
A:Description: stimulates the differentiation and proliferation of hematopoietic prog  
C:Superfamily: Interleukin-6  
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>  
F:66-72, 94-104/Disulfide bonds: #status predicted



C;Accession: A24573  
R;Nagata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y.  
Nature 319, 415-418, 1986  
A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor.  
A;Reference number: A24573; MUID:86118679; PMID:3484805  
A;Accession: A24573  
A;Molecule type: mRNA  
A;Residues: 1-207 <NAG>  
A;Cross-references: EMBL:X03438; NID:g31689; PIDN:CAA27168.1; PID:g31690  
C;Comment: This variant splice form is not expressed in three other cell lines and may have a different function.  
C;Genetics:  
A;Gene: GDB:CSF3  
A;Cross-references: GDB:119083; OMIM:138970  
A;Map position: 17q11.2-17q12  
A;Introns: 14/1; 68/3; 104/3; 153/3  
C;Superfamily: interleukin-6  
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-207/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #status predicted  
F;69-79,97-107/Disulfide bonds: #status predicted

Query Match 8.8%; Score 88.5; DB 2; Length 207;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
Matches 51; Conservative 20; Mismatches 76; Indels 53; Gaps 12;

QY 15 WTAGGAVPGGSPAWTQ-----CQ-----LSOKL---CTLANSHP-----LV 51  
DB 25 WTQV-BATPLGPASSLPQSFLKLEQVRKIQGDGAALQEKLVSECATYKLCHPPELVLL 83  
QY 52 GHMDLREGEDETTNDVPHIQCGDCGDPQGLRDNSSQFCQRIHQGLIFVEKLGSDIFTG 111  
DB 84 GH-----SLGIPWAPL-SSCPQALQ--LACGLSOLHSGFLYQGLL--QALRG 127  
QY 112 -EPSLLPDSVPVAQLHASLLGLSOLLOPEGHWHETQQLPSLPSQ-----PWQLLR 162  
DB 128 ISPELGFTLDTQLDVADEFTIWOOME-----ELGMAPALOPTQGMAPAFASAFORRAG 183  
QY 163 FKILRSLOAFVAVARFAH 182  
DB 184 VLVASHLQSGFLEVSRYLRH 203

RESULT 6  
A26496  
granulocyte colony-stimulating factor precursor - mouse  
N;Alternate names: G-CSF  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 16-Jul-1999  
C;Accession: A29536; A26496; S02493  
R;Tsuchiya, M.; Kaziro, Y.; Nagata, S.  
Eur. J. Biochem. 165, 7-12, 1987  
A;Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor.  
A;Reference number: A29536; MUID:87190474; PMID:3494605  
A;Accession: A29536  
A;Molecule type: DNA  
A;Residues: 1-208 <TSU>  
A;Cross-references: GB:X05402; NID:g51059; PIDN:CAA28986.1; PID:g51060  
R;Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986  
A;Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor.  
A;Reference number: A26496; MUID:87017003; PMID:3489940  
A;Accession: A26496  
A;Molecule type: mRNA  
A;Residues: 1-208 <TSU>  
A;Cross-references: GB:M13926; NID:g193451; PIDN:AAA37672.1; PID:g309248  
R;Simpson, R.J.; Nice, E.C.; Nicola, N.A.  
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987  
A;Title: Structural studies on the murine granulocyte colony-stimulating factor.  
A;Reference number: S02493; MUID:88106998; PMID:3501294  
A;Accession: S02493  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 31-34,'X',36-43;48-51,'X',53-57,'X',60-71;159-164,'X',166-176;183-198,'X',20

C;Genetics:  
A;Introns: 14/1; 71/3; 107/3; 156/3  
C;Superfamily: interleukin-6  
C;Keywords: cytokine; growth factor; macrophage; monomer

Query Match 8.7%; Score 87.5; DB 2; Length 208;  
Best Local Similarity 25.0%; Pred. No. 0.78;  
Matches 41; Conservative 23; Mismatches 59; Indels 41; Gaps 10;

QY 36 LSOKLCTLAWSAHP-----LVGHMDLREGEDETTNDVPHIQCGDCGDPQGLRDNSSQFCLO 91  
DB 67 LLEQLCATYKLCHPPELVLLGH-----SLGIPKASL-SGCSQALQQTQ--CUS 112  
QY 92 RIHQGLIFVEKLGSDIFTG-EPSLLPDSVPVAQLHAS-----LIGLSQLQPGG 139  
DB 113 QLHSGLCYQGLL--QALSGISPALAPTLDELQLDVANFATTIWOQMENLGVAPTQVP-- 168  
QY 140 HHWETQQ-TPSLSPSPQWQRLRLKILRSLOAFVAVARFAH 182  
DB 169 ---TOSAMPAP TSA--FORRAGGVLAISYLOGFLETARLALHH 206

RESULT 7  
A82809  
exodeoxyribonuclease V gamma chain XF0422 [imported] - Xylella fastidiosa (strain 9a5)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: A82809  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: A82809  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1121 <STM>  
A;Cross-references: GB:AE003893; GB:AE003849; NID:g9105253; PIDN:AAF83232.1; GSPDB:G82809  
A;Experimental source: strain 9a5c  
R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrelas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fajardo, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Machado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Pimenta, R.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santilli, M.; Sawa, A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.; da Silva, M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF0422

Query Match 8.6%; Score 86; DB 2; Length 1121;  
Best Local Similarity 23.7%; Pred. No. 8;  
Matches 41; Conservative 18; Mismatches 56; Indels 58; Gaps 9;

QY 22 VPGSSPANTQCCQLSOKL-----CTL-----AWSA-----HPLVGHMDLREGEDE 62  
DB 236 LPTPTKEYNGDAQPTQLRHQPTDCVTQTGENRLHWAGAGRDFTVLGSEYEVHPSGE 295  
QY 63 ETTNDVPHIQCGDCGDPQGLRDNSSQFCQRIHQGLIFVEKLGSDIFTG-----PSLLP- 117  
DB 296 ITAYDDPEQRGLTLDGGLRDS---LLQRMH-----ADLFHNSAPVAPLPA 341  
QY 118 ---DSPVAQLHASLLGLSOLL-----QPEGHWHETQQLPSLSPSQ 154  
DB 342 PRLEPDSLOFHACHTRLRELQVLHDLRLALLEPNSPEQGRFN-----PPLQPRE 390

RESULT 8

ICM56

interleukin-6 precursor - mouse

Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte growth factor

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence,revision 30-Jun-1990 #text,change 22-Jun-1999

C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S12103

R:Hanabe, O.; Akira, S.; Kamiiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.

J. Immunol. 141, 3875-3881, 1988

A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential regulatory elements in the 5' flanking region

A:Reference number: A30531; MUID:89035525; PMID:3263439

A:Accession: A30531

A:Molecule type: DNA

A:Residues: 1-211 <TAN>

A:Cross-references: GR:M20572; NID:q198369; PIDN:AAA39302.1; PID:q387386

R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Simons, J.

Eur. J. Immunol. 18, 193-197, 1988

A:Title: cDNA cloning of murine interleukin-HPI: homology with human interleukin 6.

A:Reference number: A27610; MUID:88166883; PMID:2965020

A:Accession: A27610

A:Molecule type: mRNA

A:Residues: 1-211 <VAN>

A:Cross-references: GR:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702

R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Korak, C.; Jenkins, N.A.; Copeland, N.G.; Clark, C.

J. Immunol. 142, 1372-1376, 1989

A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.

A:Reference number: A30571; MUID:89124383; PMID:2563387

A:Accession: A30571

A:Molecule type: mRNA

A:Residues: 5-211 <MO>

A:Cross-references: GR:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699

R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.

Eur. J. Biochem. 176, 187-197, 1988

A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and characterization of the cDNA

A:Reference number: S01323; MUID:88329059; PMID:3262059

A:Accession: S01323

A:Molecule type: protein

A:Residues: 25-166,'X',168-211 <SIM>

A:Note: The sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A instead of 103-T at position 168

R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.

Nucleic Acids Res. 18, 6455, 1990

A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.

A:Reference number: S12103; MUID:91057159; PMID:2243807

A:Accession: S12103

A:Molecule type: mRNA

A:Residues: 1-211 <GRE>

A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728

R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.

Biochem. Biophys. Res. Commun. 166, 139-145, 1990

A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage

A:Reference number: A30157; MUID:90147691; PMID:2302197

A:Accession: E34047

A:Molecule type: protein

A:Residues: 66-69,'X',71-75;78-94;128-148 <JA>

R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoeve, C.; Coullie, P.G.; Rubira, M.R.; Simpson, R.J.

Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986

A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine

A:Reference number: A26662; MUID:87092311; PMID:2948184

A:Accession: A26662

A:Molecule type: protein

A:Residues: 25-39,'X',41-42,'X',44-45 <VAN>

R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.

Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988

A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone

A:Reference number: A40486; MUID:89017145; PMID:3262872

A:Accession: A40486

A:Molecule type: mRNA

A:Residues: 1-211 <CHI>

A:Cross-references: GR:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410

R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; Saper, R.

Blood 72, 2070-2073, 1988

A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6

A:Reference number: A60799; MUID:89062753; PMID:3264198

A:Accession: A60799

A:Molecule type: protein

A:Residues: 77-98 <SHA>

R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.

J. Exp. Med. 171, 965-970, 1990

A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a

A:Reference number: S10241; MUID:90171860; PMID:2106569

A:Accession: S10241

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <BLA>

A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g561860

R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.

Eur. J. Biochem. 217, 53-59, 1993

A:Title: Specific covalent modification of the tryptophan residues in murine interleukin

A:Reference number: S38254; MUID:94039075; PMID:8223586

A:Accession: S38254

A>Status: preliminary

A:Molecule type: protein

A:Residues: 38-60;75,'X',77-79;176-203 <ZHA>

C:Genetics:

A:Gene: Il-6

A:Map position: 5

A:Introns: 7/1; 68/3; 106/3; 156/3

C:Superfamily: interleukin-6

C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-211/Product: interleukin-6 #status experimental <MAT>

Query Match Length DB 1; Length 211;  
Best Local Similarity 22.9%; Pred. No. 1.4;  
Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;

QY 28 PAWTCQ-----OLSKKLTAWSAHPLVGHMDLRREGDEETND--VPHIQ 72  
| | | | | : | | | | | : | | | | : | |  
Db 44 PVYTSQVGLTHVLWEIVEMRKELCN-----GNSDCMNDDALAEKNILPEIQ 94  
| | | | | : | | | | | : | | | | : | |

QY 73 CGDGDPOGLRDNOSFQRLTHQGLIYE-----KLIGSD-----I 108  
| | | | | : | | | | | : | | | | : | |

Db 95 RNDGCYQTGY--NQEICLLIKSSGLEFYSLVYMKNLNKKDKARVLQRDTFTLIHI 152  
| | | | | : | | | | | : | | | | : | |

QY 109 FTGEPSILLDPSPVAQLHASLL--GLSQILOPGEHHWFETOQIPSLSPSQWRLLFRKIL 166  
| | | | | : | | | | | : | | | | : | |

Db 153 FNQE-----VKDLHKVILPTPTSALLTD-----KLESQKEWLTKTIQFIL 194  
| | | | | : | | | | | : | | | | : | |

QY 167 RSLQAFAVAAR 178  
| | | | | : | | | | | : | | | | : | |

Db 195 KSLEEFKVTLR 206  
| | | | | : | | | | | : | | | | : | |

RESULT 9

D70537

hypothetical protein Rvll15 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: D70537

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70537

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-232 <COL>

A:Cross-references: GB:295585; GB:AL123456; NID:g3261787; PIDN:CAB09047.1; PID:e31713

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rvll15



Db 192 YRALRH 197

## RESULT 13

AG0893

aerotoxis receptor protein [imported] - Salmonella enterica subsp. enterica serovar Typhi  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 17-May-2002  
 C:Accession: AG0893  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moutle, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
 A:Reference number: AB0502; PMID:11677608  
 A:Accession: AG0893  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-506 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD07741.1; PID:g16504293; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY3395  
 C:Superfamily: methyl-accepting chemotaxis protein

Query Match 7.9%; Score 79; DB 2; Length 506;

Best Local Similarity 21.3%; Pred. No. 14;

Matches 40; Conservative 19; Mismatches 55; Indels 74; Gaps 6;

QY 48 HPLVGHMDL-----REEGDE--ETNDVPHIQCGDGDQPQ 80

| | | | | : | | | | | | | | | |

Db 53 HNLVRHPDMPKAAFAADWYTLKQGPWSGIVKRNKNGDHYVRANAVPMIREGRVTGYM 112

| | | | | : | | | | | | | | | |

QY 81 GLRD-----NSQCLQRIHOGILFYKELIGSDIFTGPELSPVPAQ 123

: | : | : | : | : | : | : | : | : |

Db 113 SIRTRAFDDIAVEPLYQALNGRCSRIHGLVVRGGLGK-----LPAMPVRW 163

: | : | : | : | : | : | : | : | : |

QY 124 LHASLGLSLLQPEGHWHWETOQIPSLSPSPQWRLL-----RFKILRSIQA 171

: | : | : | : | : | : | : | : | : |

Db 164 RVRSIMGLMAV-----LALALFGTDSWQALLGALAMLAGTALFEWQIVRPIEN 214

: | : | : | : | : | : | : | : | : |

QY 172 FVAVARV 179

| : |

Db 215 VATQALKV 222

## RESULT 14

XYCHFA

enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) - Chicken  
 N:Contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-oxoadenyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 30-Sep-1991 #sequence\_revision 12-Apr-1996 #text\_change 03-Jun-2002  
 C:Accession: S57248; S51519; A30620; A29967; A33918; A30445; A31236; B31236; A30297; A30446  
 R:Huang, W.Y.; Chirala, S.S.; Wakil, S.J.  
 submitted to the EMBL Data Library, January 1989  
 A:Description: Amino-terminal blocking group and sequence of the animal fatty acid synthase  
 A:Reference number: S57248  
 A:Accession: S57248  
 A:Molecule type: mRNA  
 A:Residues: 1-2512 <HUAL>  
 A:Cross-references: EMBL:J04485; NID:g460908; PIDN:AAB46389.1; PID:g460907  
 R:Huang, W.Y.; Chirala, S.S.; Wakil, S.J.  
 Arch. Biochem. Biophys. 314, 45-49, 1994  
 A>Title: Amino-terminal blocking group and sequence of the animal fatty acid synthase.  
 A:Reference number: S51519; MUID:95031085; PMID:7944406  
 A:Accession: S51519  
 A:Molecule type: mRNA  
 A:Residues: 1-182 <HUA2>  
 A:Cross-references: EMBL:J04485; NID:g460908  
 A:Accession: A30620

A:Molecule type: protein  
 A:Residues: 1-12 <HUA3>  
 A:Note: determination of acetylated amino end  
 R:Chang, S.I.; Hammes, G.G.  
 Biochemistry 27, 4753-4760, 1988  
 A>Title: Amino acid sequences of substrate-binding sites in chicken liver fatty acid synthase  
 A:Reference number: A29967; MUID:89000676; PMID:3167014  
 A:Accession: A29967  
 A:Molecule type: protein  
 A:Residues: 144-166; 575-583; 2141-2165 <CHAL>  
 R:Holzer, K.P.; Liu, W.; Hammes, G.G.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4387-4391, 1989  
 A>Title: Molecular cloning and sequencing of chicken liver fatty acid synthase cDNA.  
 A:Reference number: A33918; MUID:89282777; PMID:2734291  
 A:Accession: A33918  
 A:Molecule type: mRNA  
 A:Residues: 75-77, 'PV', 80-116, 'A', 118-675, 'S', 677-1169, 'N', 1171-1178, 'T', 1180-1191, 'H' L>  
 A:Accession: A30445  
 A:Molecule type: protein  
 A:Residues: 107-113; 1086-1091 <HOLI>  
 R:Yuan, Z.; Liu, W.; Hammes, G.G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 6328-6331, 1988  
 A>Title: Molecular cloning and sequencing of DNA complementary to chicken liver fatty acid synthase cDNA  
 A:Reference number: A31236; MUID:88320436; PMID:2842766  
 A:Accession: A31236  
 A:Molecule type: mRNA  
 A:Residues: 1752-2350, 'CFSSFLQ', 2351-2512 <YUAI>  
 A:Accession: B31236  
 A:Molecule type: mRNA  
 A:Residues: 1752-2512 <YUA2>  
 A:Cross-references: GB:J03860; GB:M22987; NID:g211766  
 A:Note: neither the complete nucleic acid sequence nor the complete translation are s  
 R:Chirala, S.S.; Kasturi, R.; Pazirandeh, M.; Stolow, D.T.; Huang, W.Y.; Wakil, S.J.  
 J. Biol. Chem. 264, 3750-3757, 1989  
 A>Title: A novel cDNA extension procedure. Isolation of chicken fatty acid synthase c  
 A:Reference number: A30297; MUID:89139426; PMID:2917973  
 A:Accession: A30297  
 A:Molecule type: mRNA  
 A:Residues: 1568-2512 <CHI>  
 A:Cross-references: EMBL:J04485; NID:g460908  
 A:Note: neither the complete nucleic acid sequence nor the complete translation are s  
 R:Yang, C.Y.; Huang, W.Y.; Chirala, S.; Wakil, S.J.  
 Biochemistry 27, 7773-7777, 1988  
 A>Title: Complete amino acid sequence of the thioesterase domain of chicken liver fat  
 A:Reference number: A31184; MUID:89088151; PMID:3207709  
 A:Accession: A31184  
 A:Molecule type: protein  
 A:Residues: 2209-2508 <YAN>  
 R:Kasturi, R.; Chirala, S.; Pazirandeh, M.; Wakil, S.J.  
 Biochemistry 27, 7778-7785, 1988  
 A>Title: Characterization of a genomic and cDNA clone coding for the thioesterase dom  
 A:Reference number: A31185; MUID:89088152; PMID:3207710  
 A:Accession: A31185  
 A:Molecule type: DNA  
 A:Residues: 2202-2512 <KAS1>  
 A:Cross-references: EMBL:J02839; NID:g211768; PIDN:AAA82106.1; PID:g211769  
 A:Accession: A30446  
 A:Molecule type: mRNA  
 A:Residues: 2202-2512 <KAS2>  
 A:Cross-references: EMBL:J02839; NID:g211768  
 A:Note: the translated sequence in Genbank entry CHKFASA, release 113.0, PIDN:AAA8210  
 wn in Fig. 5  
 R:Huang, W.Y.; Stoops, J.K.; Wakil, S.J.  
 Arch. Biochem. Biophys. 270, 92-98, 1989  
 A>Title: Complete amino acid sequence of chicken liver acyl carrier protein derived f  
 A:Reference number: S03856; MUID:89192401; PMID:2648999  
 A:Accession: S03856  
 A:Molecule type: protein  
 A:Residues: 2121-2209 <HUA4>  
 R:Chang, S.I.; Hammes, G.G.  
 Biochemistry 28, 3781-3788, 1989  
 A>Title: Amino acid sequences of pyridoxal 5'-phosphate binding sites and fluorescenc





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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:59 ; Search time 7.85455 Seconds  
(without alignments)  
998.024 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRVAILMLLLPWTFAQR.....QAFVAARVFAHGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	CSF3_PIG	106.5	10.6	195	1	002837 sus scrofa
2	CSF3_FELCA	99.5	9.9	194	1	002708 felis silve
3	IL6_SHEEP	96	9.6	208	1	P23455 ovis aries
4	CSF3_SHEEP	90.5	9.0	174	1	Q28746 ovis aries
5	CSF3_CANFA	89.5	8.9	175	1	P35834 canis fami
6	IL6_CAPHI	89	8.9	208	1	Q28319 capra hircu
7	CSF3_HUMAN	88.5	8.8	207	1	P09919 homo sapien
8	CSF3_MOUSE	87.5	8.7	208	1	P09920 mus musculu
9	IL6_MOUSE	85	8.5	211	1	P08505 mus musculu
10	CSF3_BOVIN	80.5	8.0	195	1	P35833 bos taurus
11	PRZ3_DROME	79.5	7.9	201	1	077438 drosophila
12	MGF_CHICK	79	7.9	2511	1	P13834 gallus gall
13	FAS_CHICK	78.5	7.8	208	1	P12276 gallus gall
14	IL6_FELCA	78.5	7.8	208	1	P41683 felis silve
15	AT10_MOUSE	78.5	7.8	450	1	P58459 mus musculu
16	RMUC_VIBCH	77.5	7.7	513	1	Q9KVG7 vibrio chol
17	CAFA_HUMAN	75.5	7.5	938	1	Q13111 homo sapien
18	IL6_ORCOR	75	7.5	205	1	Q28747 orcinus orc
19	IL6_RAT	75	7.5	211	1	P20607 rattus norv
20	DHGA_ALICA	75	7.5	801	1	P05465 acinetobact
21	IL6_PIG	74.5	7.4	212	1	P26893 sus scrofa
22	TNFB_MACEU	73.5	7.3	201	1	Q9XT48 macropus eu
23	IL6_CANFA	73.5	7.3	207	1	P41323 canis fami
24	6PGL_MYCTU	73.5	7.3	247	1	O06814 mycobacteri
25	BPHY_DEIRA	73.5	7.3	755	1	Q9RZA4 deinococcus
26	BGAL_ARTSP	73.5	7.3	1015	1	Q59140 arthrobacte
27	KG3H_DROME	72	7.2	501	1	P83101 drosophila
28	GLS1_ECOLI	71.5	7.1	310	1	P77454 escherichia
29	IL6_BOVIN	71	7.1	208	1	P26892 bos taurus
30	IL6_CERTO	71	7.1	212	1	P46650 cercopithec
31	KPYK_METEX	71	7.1	483	1	O05118 methylobact
32	ELF1_HUMAN	71	7.1	619	1	P32519 homo sapien
33	IND1_HUMAN	70	7.0	195	1	P37290 homo sapien

34 70 7.0 427 1 THIL\_HUMAN P24752 homo sapien  
35 70 7.0 726 1 AD20\_HUMAN O43506 homo sapien  
36 70 7.0 812 1 PDA1\_ORYSA O43007 oryza sativ  
37 70 7.0 1538 1 LHR\_ECOLI P30015 escherichia  
38 69.5 6.9 208 1 IL6\_HORSE Q95181 equus caball  
39 69.5 6.9 430 1 KDTA\_CHIMU Q9PK15 chlamydia m  
40 69.5 6.9 514 1 G6PD\_MYCTU O08407 mycobacteri  
41 69.5 6.9 1396 1 VCAP\_VZVD P09245 varicella-z  
42 69.5 6.9 1544 1 TUSP\_HUMAN Q9NRJ4 homo sapien  
43 69 6.9 234 1 NK4\_HUMAN P24001 homo sapien  
44 69 6.9 592 1 FTSZ\_BARBA O31314 bartonella  
45 69 6.9 639 1 AMYG\_ASPAK P23176 aspergillus

#### ALIGNMENTS

RESULT 1  
CSF3\_PIG  
ID CSF3\_PIG STANDARD; PRT; 195 AA.  
AC O02837; O19180;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Granulocyte colony-stimulating factor precursor (G-CSF).  
GN CSF3.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kumburg P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Gloster S.E., Sandeman R.M., Strom A.D.G.;  
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony  
stimulating factor.";  
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE  
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,  
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS  
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS  
CSF INDUCES GRANULOCYTES (BY SIMILARITY).  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: O-GLYCOSYLATED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; Y10494; CAA71518.1; -;  
DR EMBL; U68482; AAB70701.1; -;  
DR EMBL; U68481; AAB70700.1; -;  
DR HSSP; P35833; 1BCG.  
DR InterPro; IPR003629; GCSF\_MGF.  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR pfam; PF00489; IL6; 1.  
DR PRINTS; P800433; IL6GCSFMGF.  
DR PRODOM; P008388; GCSF\_MGF; 1.  
DR SMART; SM00126; IL6; 1.  
DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 195 GRANULOCYTE COLONY-STIMULATING FACTOR.

```

FT DISULFID      57    63          BY SIMILARITY.
FT DISULFID      85    95          BY SIMILARITY.
FT CARBOHYD     154   154          O-LINKED (GALNAC... ) (BY SIMILARITY).
FT CONFLICT     123   123          A -> R (IN Ref. 1).
SQ SEQUENCE     195 AA: 21214 MW: 84787F20DB0AEA1C CRC64:

Query Match              10,68: Score 106.5; DB 1; Length 195;
Best Local Similarity    24.98; Pred.No. 0.0044;
Matches 52; Conservative 28; Mismatches 76; Indels 53; Gaps 10;

QY 7 VMLLLLPTAGRAVPGGS--SPAWTQCQ-----OLSKKLCITLAWS 46
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 LMAQLLLWHIALMVMPPAAPLSPASSIPQSFLLKCLEQVRKTKADGAELQRCLCATKL 62
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 47 AHP- ---LVGHMDLRREGDEETNDVPHIOCGDGCDPQGLRDNDSQFCIORIHOGLIIFYEK 102
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 CHPQEVLVLGH-----SUGLPQASL-SSCSSQALQLTG--CLNQZHGGLVLTQG 108
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 103 LIGSDIFTGG-EPSLDPDSPVAQLHASLGLISQLLPQEGHHWETQQIPTSLSPSQ----- 154
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 109 LL-QALGISPELAPALDIQLQDVDTLATNIWLME---DLRMAPASLPTQGTVPVTF 162
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
QY 155 -PWORLLIRFKILRSLOAFVAAARVEAH 182
   :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 SAFQRAGGVVVSQLSFLELAYRVLYR 191
   :| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
CSF3_FELCA
ID CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 20-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
GN CSF3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-European shorthair; TISSUE=Lung;
RA Dunham S.P., Onions D.E.;
RT *cloning, sequence and expression of feline granulocyte colony
RT stimulating factor.*;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: GRANULOCTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
CC EMBL; Y08558; CAA69853.1; -.
CC HSPSP; P35834; LBGE.
CC InterPro; IPR003629; GCSF_MGF.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC ProDom; PD008388; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.

```



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DR PDB; 1BGE; 31-OCT-93.
DR InterPro: IPR003629; GCSF_MGF.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008368; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Glycoprotein; 3D-structure.
DR FT DISULFID 37 43
FT CARBOHYD 65 75
FT HELIX 134 134
FT HELIX 12 40
FT TURN 45 47
FT TURN 48 48
FT TURN 49 55
FT TURN 56 56
FT TURN 63 65
FT TURN 67 68
FT TURN 72 92
FT TURN 93 95
FT TURN 98 100
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FT HELIX 144 171
FT TURN 172 172
FT STRAND 173 173
SQ SEQUENCE 175 AA; 18858 MW; 28C26B24990C6DB3 CRC64;

Query Match 8.9%; Score 89.5; DB 1; Length 175;
Best Local Similarity 24.7%; Pred. NO. 0.16;
Matches 40; Conservative 21; Mismatches 68; Indels 33; Gaps 8;

QY 36 LSKKLTLSAHP-----LVGHMDLREEGDETTNDVPHIOGDCGDPQGLRDNQSQCLO 91
DB 32 LQETLCATHQLCPHELVLGH-----ALGIFQPPPL-SCSSQALQ--LMGCLR 77
QY 92 RIHQGLIFYEKLGSDFITG-EPSLLPDSFVAQLHASLGLSOLLQSGHGWETQQTIPS 150
DB 78 QLSHGLFLYGGLL--QALAGISPELAPTLDLTQLDTPFAINWQOME-----DLGMAPV 131
QY 151 SPQO-----PQORLLRFKILRSLOAFVAVARVAFHGA 184
DB 132 PPIQGTMPAFTSAFQRAGGVLVASNLQSFLELAYRALRHFA 173

RESULT 6
IL6_CAPHI
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC 028319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; PubMed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
cells.";
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC -FUNCTIONS; IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC
DR EMBL; D86569; BAA13118.1; -
DR HSSP; P05331; IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29
FT CHAIN 30 208
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 38 38
FT SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 8.9%; Score 89; DB 1; Length 208;
Best Local Similarity 24.1%; Pred. NO. 0.21;
Matches 48; Conservative 27; Mismatches 90; Indels 34; Gaps 7;

QY 6 AVMLLLLPWTAGRAVPGSGSPAMTQCQLSKLTLSAHPVLGHM-----DL 56
DB 13 AVSLGLLLWMTS-AFTPGCLGEDFKNTTPSRULLTTPTEALIKHIVDKISAIRKEI 71
QY 57 REGDP-----ETNDVPHIOGDCGDPQGLRDNQSQCLORIHQGLIFYEKLGL-- 105
DB 72 CEKNDCEKSKETLAENKILKPKMEKDGKQSGF--NOAICLIKTTAGLLEYQIYLDLF 129
QY 106 SDITCEPSLLPDSFVAQLHASLGLSOLLQSGHGWETQQTIPSLSQSPQWR 159
DB 130 QNEFEGN-----QEVMELOSSIRTLQILKEKTAGLTTTATNTDMLERKQSSNEWVK 184
QY 160 LLRFKILRSLOAFVAVAR 178
DB 185 AKVIIILRSLENFLQFSLR 203

RESULT 7
CSF3_HUMAN
ID CSF3_HUMAN STANDARD; PRT; 207 AA.
AC P09919;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
DE (Filgrastim) (lenograstim).
GN CSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118679; PubMed=3484805;
RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
RT "Molecular cloning and expression of cDNA for human granulocyte
RT colony-stimulating factor.";
RL Nature 319:415-418(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86220137; PubMed=2423327;

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RN SEQUENCE OF 25-211.  
 RX MEDLINE=88329059; PubMed=3262059;  
 RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;  
 RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid  
 RL sequence and relation to human interleukin-6.";  
 RL Eur. J. Biochem. 176:187-197(1988).  
 [8]  
 RN SEQUENCE OF 66-75; 78-84 AND 128-148.  
 RX MEDLINE=90147691; PubMed=2302197;  
 RA Jahnke W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;  
 RT "Internal amino acid sequencing of proteins by in situ cyanogen  
 bromide cleavage in polyacrylamide gels.";  
 RL Biochem. Biophys. Res. Commun. 166:139-145(1990).  
 [9]  
 RN SEQUENCE OF 25-45.  
 RX MEDLINE=87092311; PubMed=2948184;  
 RA van Snick J., Cayphas S., Vink A., Uytendhove C., Coulie P.G.,  
 RA Rubira M.R., Simpson R.J.;  
 RT "Purification and NH2-terminal amino acid sequence of a  
 RT T-cell-derived lymphokine with growth factor activity for B-cell  
 RT hybridomas.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).  
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL  
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION  
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND  
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN  
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; X06203; CAA29560.1; -  
 DR EMBL; M20572; AAA39302.1; -  
 DR EMBL; X51457; CAA35824.1; -  
 DR EMBL; J03783; AAA39301.1; -  
 DR EMBL; X54542; CAA38411.1; -  
 DR EMBL; M24221; AAA68814.1; -  
 DR PIR; A30531; ICM56.  
 DR HSSP; P05231; 1ALU.  
 DR MGD; MGI:96559; IL6.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR InterPro; IPR003574; Interleukin\_6.  
 DR Pfam; PF00489; IL6; 1  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR ProDom; PD004356; Interleukin\_6; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 DR Cytokine; Growth factor; Glycoprotein; Signal.  
 KW SIGNAL 1 24  
 FT CHAIN 25 211 INTERLEUKIN-6.  
 FT DISULFID 70 76 BY SIMILARITY.  
 FT DISULFID 99 109 BY SIMILARITY.  
 SQ SEQUENCE 211 AA; 24384 MW; BBB47DDA9E66787A CRC64;  
 Query Match 8.5%; Score 85; DB 1; Length 211;  
 Best Local Similarity 22.9%; Pred. No. 0.51;  
 Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;  
 QY 28 PAWTQCQ-----OLSKLCTLAWSAHLVGHMDLREGEDETTND--VPHIQ 72  
 DB 44 PYVITSQVGLITHVLWEIVEMRKELCN-----GNSDCMNDALAEENLKLPEIQ 94  
 QY 73 CGDGDPOGLRNSQFCLQRHOGILFEY-----KLLGSD-----I 108  
 DB 95 RNDGCGYQTCY--NQEICLLKISSGLLEYHSYLEYMKNNLKNKKARVLRQDRTTLHI 152

QY 109 FTGERSLPLDSPAQLHASLL--GLSQLQPEGHWHWETQIPLSPSQPWQRLLLRKIL 166  
 DB 153 FQOE-----VKDLHKVILVPTFISNALLTD-----KLESQKELWRTKTIQFIL 194  
 QY 167 RSLQAFVAVAAR 178  
 DB 195 KSLEEFELKVTLR 206  
 RESULT 10  
 CSF3\_BOVIN  
 ID CSF3\_BOVIN STANDARD; PRT; 195 AA.  
 AC P35833; Q9TV89;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Granulocyte colony-stimulating factor precursor (G-CSF).  
 GN CSF3 OR GCSF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein;  
 RA Heidari M., Kehrli M.E. Jr.;  
 RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte  
 RT colony stimulating factor.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RP MEDLINE=94076341; PubMed=7504736;  
 RX Lovejoy B., Cascio D., Eisenberg D.;  
 RT "Crystal structure of canine and bovine granulocyte-colony  
 RT stimulating factor (G-CSF).";  
 RL J. Mol. Biol. 234:640-653(1993).  
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE  
 CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,  
 CC DIFFERENTIATION AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS,  
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS  
 CC CSF INDUCES GRANULOCYTES.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: O-GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; AF092533; AAD16102.1; -  
 DR FDB; I6CC; 31-OCT-93; -  
 DR InterPro; IPR003629; GCSF\_MGF.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR Pfam; PF00489; IL6; 1.  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR ProDom; PD008388; GCSF\_MGF; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 DR Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.  
 KW SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 195 GRANULOCYTE COLONY-STIMULATING FACTOR.  
 FT DISULFID 57 63  
 FT DISULFID 85 95  
 FT CARBOHYD 154 154  
 FT CONFLICT 93 94 O-LINKED (GALNAc...) (BY SIMILARITY).  
 FT HELIX 32 60 TS -> RG (IN REF. 2).

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FT HELIX 65 69
FT TURN 70 71
FT HELIX 72 75
FT TURN 76 76
FT HELIX 83 85
FT TURN 87 89
FT HELIX 92 112
FT TURN 113 115
FT TURN 118 120
FT HELIX 121 145
FT HELIX 164 191
FT TURN 192
SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 8.0%; Score 80.5; DB 1; Length 195;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 48; Conservative 25; Mismatches 79; Indels 53; Gaps 11;

QY 7 VMLLLLPWTAQ-----GRAVPGSSPAWTO-----C-----QQLSQKLCTLAWS 46
DB 3 LMLVQLLWHSALMTVHEATPLGPARSLPQSFLLKCLEQVRKIQADGAELQERLCAHKL 62
QY 47 AHP-----LVGHMDLREEDETTNDVPHIQCGDCGDPGLRDNDSQFCLORIHOGILFIYEK 102
DB 63 CHPELMLLRH-----SLGIPQAPL-SSCSQSLSQLTSS--CLNQLHGLGLFIYQG 108
QY 103 LIGSDIFTG-FPSLLPDSFVAQLHASLLGLSOLLQPEGHWHWETOQIPSLSPSQ----- 154
DB 109 LL--QALAGISPELAPTLDLTOLDVDFATNIWLQME-----DLGAAPAVQPTQGMATFTT 162
QY 155 -PWQRLLLRFKILRSLOAFVAAR 178
DB 163 SAFQRRAGGVLVASQLHRELEAYR 187

RESULT 11
FRZ3_DROME STANDARD; PRT; 581 AA.
AC Q77438; Q91727; Q9NTU0; Q9U902; Q9W5D5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled protein 3 precursor (Frizzled-3) (DFz3).
GN DF3 OR EG:34F3.6 OR CG16785.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; PubMed=10498678;
Sato A., Koilna T., Ui-Tei K., Miyata Y., Saigo K.;
RT "dfizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
of Wingless signaling in wingless hypomorphic mutants.";
RL Development 126:4421-4430(1999).
[2]
RN RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=20171076; PubMed=10704878;
Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The wingless target gene dfz3 encodes a new member of the Drosophila
Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
[3]
RN RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=107311137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Borkova D.,
Dreano S., Gloux S., Letaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papaqiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
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RA Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the x chromosome of D.
RL Science 287:2220-2222(2000).
[4]
RN RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=107311132;
Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter F.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibagwan C.,
RA Jalali M.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[1]
RN RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; PubMed=10498678;
Sato A., Koilna T., Ui-Tei K., Miyata Y., Saigo K.;
RT "dfizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
of Wingless signaling in wingless hypomorphic mutants.";
RL Development 126:4421-4430(1999).
[2]
RN RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=20171076; PubMed=10704878;
Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The wingless target gene dfz3 encodes a new member of the Drosophila
Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
[3]
RN RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=107311137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Borkova D.,
Dreano S., Gloux S., Letaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papaqiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
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SEQUENCE FROM N.A.

TISSUE=Lymphocytes;

MEDLINE=94052249; PubMed=8234373;

Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;

"Molecular cloning and characterization of a cDNA encoding feline interleukin-6,"

Proc. Soc. Exp. Biol. Med. 204:301-305(1993).

-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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EMBL; I16914; AAA16620.1; --  
EMBL; D13227; BA02507.1; --  
HSPB; P05231; IL6.  
InterPro: IPR003573; IL6\_MGF\_GCSF.  
InterPro: IPR003574; Interleukin\_6.  
Pfam: PF00489; IL6; 1.  
PRINTS: PR00433; IL6GCSFMGF.  
ProDom: PD004356; Interleukin\_6; 1.  
SMART: SM00126; IL6; 1.  
PROSITE: PS0254; INTERLEUKIN\_6; 1.  
Cytokine; Glycoprotein; Growth factor; Signal.  
FT SIGNAL 1 27 POTENTIAL..  
FT CHAIN 28 208 INTERLEUKIN-6.  
FT DISULFD 68 74 BY SIMILARITY..  
FT DISULFD 97 107 Y SIMILARITY..  
FT FT CONFLICT 2 2 T -> N (IN REF. 2).  
FT FT CONFLICT 45 45 S -> P (IN REF. 2).  
FT FT CONFLICT 133 133 E -> K (IN REF. 2).  
FT FT CONFLICT 173 187 AKLOSQEEWLRTTTI -> LCSCHRRVAAEHNH (IN  
REF. 2).  
FT FT CONFLICT 200 201 FS -> LR (IN REF. 2).  
SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;  
  
Query Match 7.8%; Score 78.5; DB 1; Length 208;  
Best Local Similarity 25.4%; Pred. No. 2.1;  
Matches 34; Conservative 19; Mismatches 60; Indels 21; Gaps  
  
Qy 58 EGDEETNDVPHTCGDGDGPGLRNSQCFLRIHQGL---IFXEKLIGSDIFTGPS 114  
Db 78 KEALENNLLPKIAEKGCQSGFG--NQETLTRITTLGLEFIYLKFL-QDKYEGR-- 132  
Qy 115 LLPDSPVAQLHASLGLSQLLPQEGHHWETQIP-----SLSPQPQRLLLLRFK 164  
Db 133 ---EENAKSVYSTNVLLQMLKRKGKNODEVTIPVPTVEVLGAKLOEQEWELRHTTHL 189  
Qy 165 ILRSQAFAVAAR 178  
Db 190 TURLEDLFQFSLR 203  
  
RESULT 15  
AT10\_MOUSE  
ID AT10\_MOUSE STANDARD; PRT; 450 AA.  
AC P58459:  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE ADAMTS-10 (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 10) (ADAM-TS 10) (ADAM-TS10) (Fragment).  
GN ADAMTS10.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Seidin M.F., Apté S.S.;  
RT "A novel gene of the ADAMTS family predicts ADAMTS-10, a  
RT metalloprotease with unique structural features and expression  
RT pattern.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular  
CC matrix (By similarity).  
CC -1- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT  
CC FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By  
CC similarity).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.  
CC -1- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF302012; AAK97226.1; -  
DR InterPro; IPR000884; TSP1.  
DR SMART; SM00209; TSP1; 4.  
DR PROSITE; PS50092; TSP1; 1.  
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Repeat;  
KW Extracellular matrix.  
FT NON\_TER 1 1  
FT DOMAIN <1 51 CYS-RICH.  
FT DOMAIN 52 174 SPACER.  
FT DOMAIN 171 232 TSP TYPE-1 1.  
FT DOMAIN 234 290 TSP TYPE-1 2.  
FT DOMAIN 294 348 TSP TYPE-1 3.  
FT DOMAIN 353 399 TSP TYPE-1 4.  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 450 AA; 48861 MW; 2377D0E2CFBFBFCA CRC64;

Query Match 7.8%; Score 78.5; DB 1; Length 450;  
Best Local Similarity 24.2%; Pred. No. 5;  
Matches 36; Conservative 13; Mismatches 69; Indels 31; Gaps 6;  
QY 14 PWTAGRAVPGSSPAWTCQQLSKLCTLAWSAHLPLVGHMDLREEGDEETNDVP---- 69  
DB 179 PWTKCSAQCAGSQVQVVECR---NQLDSSAVAPHYCSGHKLPKROKACNTEPCPDWV 235  
QY 70 ---HTQCGDGDQGLRDNQSFQRIHQGLIFYEKILGLGSDIFTGEPSLLPDSVAQLHA 126  
DB 236 VGNWRSRCSRSCD-AGVRSRSVVCQRRVS-----AAEEKALDDSDACPOPRP 279  
QY 127 SLLGLSQ--LLOPEGHWHWTQIPLSPS 153  
DB 280 PVLEACQGMCPPE---WATLDWSECTPS 305

Search completed: November 20, 2002, 11:53:24  
Job time : 9.85455 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:20 ; Search time 26.0182 Seconds  
(without alignments)  
1496.757 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRAYMLLLLPWTAQR.....QAFVAARVFAGHAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phase: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1004	100.0	189	4 Q9H2A5	Q9H2A5 homo sapien
2	1000	99.6	189	4 Q9NPF7	Q9NPF7 homo sapien
3	846	84.3	193	6 Q9N2H9	Q9N2H9 sus scrofa
4	784.5	78.1	196	11 Q91Z84	Q91Z84 rattus norv
5	718.5	71.6	196	11 Q9EQ14	Q9EQ14 mus musculus
6	97	9.7	195	6 Q9GJU0	Q9GJU0 felis silve
7	86	8.6	1121	16 Q9PC80	Q9PC80 xylella fas
8	85.5	8.5	352	15 Q9PZ44	Q9PZ44 multiple sc
9	85.5	8.5	363	4 Q9NR24	Q9NR24 homo sapien
10	84.5	8.4	210	11 Q9WVQ8	Q9WVQ8 mesocricetu
11	83	8.3	137	15 Q9PZ45	Q9PZ45 multiple sc
12	82	8.2	208	6 Q9XT80	Q9XT80 delphinapte
13	82	8.2	858	11 Q923K0	Q923K0 mus musculus
14	81.5	8.1	212	11 Q91ZL3	Q91ZL3 sigmodon hi
15	81.5	8.1	540	6 Q95K25	Q95K25 macaca fasc
16	80.5	8.0	232	16 O06567	O06567 mycobacteri

17	80.5	8.0	530	10 Q9C9S0	Q9C9S0 arabidopsis
18	80	8.0	215	11 Q91ZK6	Q91ZK6 sigmodon hi
19	80	8.0	324	13 Q90255	Q90255 scophthalmu
20	80	8.0	506	16 Q82LX8	Q82LX8 salmonella
21	80	8.0	633	13 Q90256	Q90256 scophthalmu
22	80	8.0	858	11 Q925D9	Q925D9 mus musculu
23	80	8.0	858	11 Q925D8	Q925D8 mus musculu
24	80	8.0	858	11 Q925A4	Q925A4 mus musculu
25	80	8.0	858	11 Q91VA4	Q91VA4 mus musculu
26	80	8.0	922	4 Q9HCG7	Q9HCG7 homo sapien
27	80	8.0	927	4 Q96SU2	Q96SU2 homo sapien
28	80	8.0	927	4 Q96A51	Q96A51 homo sapien
29	79.5	7.9	328	13 Q9YHX3	Q9YHX3 brachydanio
30	79.5	7.9	472	10 Q9LXK3	Q9LXK3 hordeum vul
31	79.5	7.9	1135	5 Q9VJF6	Q9VJF6 drosophila
32	79	7.9	134	4 Q96NR2	Q96NR2 homo sapien
33	79	7.9	506	16 Q823M0	Q823M0 salmonella
34	79	7.9	786	2 P95466	P95466 pantoea cit
35	78.5	7.8	207	6 Q9MYZ7	Q9MYZ7 canis fami
36	78.5	7.8	541	4 Q96AR2	Q96AR2 homo sap
37	78.5	7.8	1317	15 Q9WHI8	Q9WHI8 walleye
38	78	7.8	379	5 Q95WF6	Q95WF6 acropora m
39	78	7.8	457	10 Q9AUV3	Q9AUV3 oryza sativ
40	78	7.8	510	2 Q93TX3	Q93TX3 stigmatella
41	78	7.8	1026	10 Q49529	Q49529 arabidopsis
42	78	7.8	1820	4 Q9P2B6	Q9P2B6 homo sapien
43	77.5	7.7	967	10 Q80540	Q80540 arabidopsis
44	76.5	7.6	399	16 Q8YY64	Q8YY64 anabaena sp
45	76.5	7.6	881	17 Q9HMG9	Q9HMG9 halobacteri

## ALIGNMENTS

RESULT 1

Q9H2A5	PRELIMINARY:	PRT:	189 AA.
ID Q9H2A5;			
AC Q9H2A5;			
DT 01-WAR-2001 (TREMBLrel. 16, Created)			
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Interleukin 23 p19 subunit.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20567322; PubMed=11114383;			
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,			
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,			
RA Liu M.-R., Gorman D., Wagner J., Zukowski S., Liu Y.-J., Abrams J.S.,			
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,			
RA Kastelein R.A.;			
RT "Novel p19 protein Engages IL-12p40 to Form a Cytokine, IL-23, with			
RT Biological Activities Similar as Well as Distinct from IL-12.";			
RL Immunity 13:715-725(2000).			
DR EMBL; AF301620; AAG37232.1; -			
DR InterPro; IPR003573; IL6_MGF_GCSF.			
DR SMART; SM00126; IL6; 1.			
SQ SEQUENCE 189 AA: 20744 MW; BFB5C0F42D4C1E3A CRC64;			

Query Match	100.0%	Score 1004;	DB 4;	Length 189;
Best Local Similarity	100.0%	Pred. No. 7.2e-96;		
Matches 189;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1 MLGSRAYMLLLLPWTAQR	AVPGGSSPAWTCQQLSQKLT	LAWSAHPVGHMDLREEG	60	
Db 1 MLGSRAYMLLLLPWTAQR	AVPGGSSPAWTCQQLSQKLT	LAWSAHPVGHMDLREEG	60	
QY 61 DEETNDVPHIQCGDCGCDPQGLR	NSQFCLQRIHQGLIFYEKLLGS	DIFTFGEPSLLPDS	120	
Db 61 DEETNDVPHIQCGDCGCDPQGLR	NSQFCLQRIHQGLIFYEKLLGS	DIFTFGEPSLLPDS	120	

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QY 121 VAQLHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
|||||
Db 121 VAQLHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
QY 181 AHGAATLSP 189
|||||
Db 181 AHGAATLSP 189

RESULT 2
Q9NPF7 Q9NPF7 PRELIMINARY; PRT; 189 AA.
AC Q9NPF7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SGRF precursor.
GN SGRF
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN.
RA Hirata Y., Kosuge Y.;
RT "SGRF; a novel member of the IL-6/G-CSF family.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030000; BAA93686.1; -.
DR EMBL; AB030001; BAA93687.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
DR Signal.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 189 SGRF.
SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;

Query Match 99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 1.9e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60
|||||
Db 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60
QY 61 DEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLLPDS 120
|||||
Db 61 DEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLLPDS 120
QY 121 VAQLHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
|||||
Db 121 VAQLHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
QY 181 AHGAATLSP 189
|||||
Db 181 AHGAATLSP 189

RESULT 3
Q9N2H9 Q9N2H9 PRELIMINARY; PRT; 193 AA.
AC Q9N2H9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SGRF.
GN SGRF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Hirata Y., Kosuge Y.;
RT "SGRF; a novel member of the IL-6/G-CSF family.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030002; BAA93688.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 193 AA; 21132 MW; 05F28DE94810B9E1 CRC64;

Query Match 84.3%; Score 846; DB 6; Length 193;
Best Local Similarity 85.4%; Pred. No. 1.6e-79;
Matches 164; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDL- 56
|||||
Db 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDL- 56
QY 57 REEGDEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLL 116
|||||
Db 61 REEGDEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLL 120
QY 117 PDSPVAQHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAV 176
|||||
Db 121 PDSPVAQHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAV 180
QY 177 ARVFAHGAATLS 188
|||||
Db 181 ARVFAHGAATLS 192

RESULT 4
Q91284 Q91284 PRELIMINARY; PRT; 196 AA.
AC Q91284;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Interleukin 23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW;
RA Tran G., Hodgkinson S.;
RT "Rattus norvegicus IL-23 mRNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY053379; AAL18229.1; -.
SQ SEQUENCE 196 AA; 21986 MW; 188FF74BC409A961 CRC64;

Query Match 78.1%; Score 784.5; DB 11; Length 196;
Best Local Similarity 79.4%; Pred. No. 3.7e-73;
Matches 150; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDL-REE 59
|||||
Db 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSOKLCTLAWSAHLVGHMDL-REE 60
QY 60 GDEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLLPDS 119
|||||
Db 61 GDEETTNDVPHIQCGDCGDPQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTGPEPSLLPDS 120
QY 120 PVAQLHASLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARV 179
|||||
Db 121 PVDQLHTSLLGLSLLQLOPEGHWHWETQOIPSLSPSPQWQRLRLFKILRSLOAFVAVARV 180
QY 180 FAHGAATLS 188
|||||
Db 181 FAHGAATLS 189

RESULT 5
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Q9EQ14
ID Q9EQ14 PRELIMINARY; PRT; 196 AA.
AC Q9EQ14;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 23 p19 subunit (Interleukin 23, alpha subunit p19).
GN IL23A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20567322; PubMed=11144383;
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 protein Engages IL-12p40 to Form a Cytokine, IL-23, with
RT Biological Activities Similar as Well as Distinct from IL-12.";
RL Immunity 13:715-725(2000).
[2]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF301619; AAG37231.1; -.
DR EMBL; BC019953; AAH19953.1; -.
DR MGD; MGI:1932410; IL23a.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;

Query Match 71.6%; Score 718.5; DB 11; Length 196;
Best Local Similarity 74.6%; Pred. No. 2.5e-66;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLGSRVAVMLLLPMTAGRAVPGGSSPAWTQCQQLSOKLCTLAWSAHLVGHMD-LREE 59
  || |||||:| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1 MLDCRAVIMLLPWPVTOGLAVPRSSSPDQAQQQLSRNLCMLAWNAHAPAGHNNLLREE 60
  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 60 GDEETNVPHIQCGDCDQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGSPSLPDS 119
  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 61 EDEETNNVPRIQCDCDQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGSPSLPDS 120
  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 120 PVAQLHASLGLSLLQLLQEGHGHWTQIQPSLSPSQWQRLRLFKILRSQAFAVAARV 179
  1: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 PWEQLTSLGLSLLQLLQEGHGHWTQIQPSLSPSQWQRLRLFKILRSQAFAVAARV 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 180 FAHGAATLS 188
  ||||| |||||
Db 181 FAHGAATLT 189

RESULT 6
Q9GJU0
ID Q9GJU0 PRELIMINARY; PRT; 195 AA.
AC Q9GJU0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN G-CSF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
RN SEQUENCE FROM N.A.
RA Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline

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RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042552; BABI7789.1; -.
DR EMBL; AB042553; BABI7757.1; -.
DR HSP; P35834; IBGE.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSF_MGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412FCF CRC64;

Query Match 9.7%; Score 97; DB 6; Length 195;
Best Local Similarity 23.9%; Pred. No. 0.044;
Matches 47; Conservative 25; Mismatches 75; Indels 50; Gaps 11;

QY 15 WTAQGRAVPGGSSPAWTQ-----CQ-----LSQKLCITLAWSAHP----LVGHM 54
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 WMYQ-EATPLGPTSSUPQSFLKLEQVRKVQADGTALQERLCAAHKLCHPEELVLGH- 73
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 55 DLREEGDEETNDVPHIQCGDCDQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTG-EP 113
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 -----ALGIPQAPL-SSCSQALQLTG--CLRLHSLGLYQGLL--QALAGISP 118
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 114 SLLPSPVAQLHASLGLSLLQLLQEGHGHWTQIQPSLSPSQ-----PWQRLRLRFKI 165
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 ELAPTLDMLQLDITDFAINIQOME---DVGMAFAPVPTQTGTMPTTSAFORAGTGV 174
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 166 LRSQAFAVAARVFAH 182
  :|:|:|:| | | | | | |
Db 175 ASNLQSFLEVAYRALRH 191

RESULT 7
Q9PG80
ID Q9PG80 PRELIMINARY; PRT; 1121 AA.
AC Q9PG80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Exodeoxyribonuclease V gamma chain.
GN XF0422.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Itaga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.B., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,

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Db	8	WQDCDTQTLRKKRIFFCSTAMPQYPLQGRETWLPGESNYNIIQLDLFCRKEGKWSV	67		
QY	69	PHIQCGDCDPOGLRNSQFCQLRIHQGLIFYEKLGLGSDIFTGEPSLLP-----DSPVAQ	123		
Db	68	PYVQTF-----FSLRNSQLC-----KKCGL-CPTGSPQSPPPYPVSPVSPPTS	109		
QY	124	LHASLGLLSQLQPE-----GHHWETQOIPSLSPSQ	154		
Db	110	STNRKDPPLTQTQVQKEIDKGVNNEPKSANIPRLCPLQ	145		
RESULT 9					
Q9NRZ4	PRELIMINARY; PRT; 363 AA.				
AC	Q9NRZ4;				
DT	01-OCT-2000 (TReMBLrel. 15, Created)				
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)				
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)				
DE	Gag.				
GN	GAG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20284713; PubMed=10826480;				
RA	Volset C., Bouton O., Bedin F., Duret L., Mandrand B., Mallet F.,				
RA	Paranhos-Baccala G.;				
RT	"Chromosomal distribution and coding capacity of the human endogenous				
RT	retrovirus HERV-W family.";				
RL	AIDS Res. Hum. Retroviruses 16:731-740(2000).				
DR	EMBL: AF156961; AAF74213.1; -				
DR	InterPro: IPR000840; Gag_MA.				
DR	InterPro: IPR003036; Gag_p30.				
DR	Pfam: PF01140; Gag_MA; 1.				
DR	Pfam: PF02093; Gag_p30; 1.				
SQ	SEQUENCE 363 AA; 41075 MW; C654B4BDA473785AB CRC64;				
Query Match 8.5%; Score 85.5; DB 4; Length 363;					
Best Local Similarity 24.6%; Pred. No. 1.4;					
Matches 45; Conservative 13; Mismatches 50; Indels 75; Gaps					
QY	19	GRAVPGGSSPA-----WTQC--QOLSQK-----LCTLAWSAHPLVGHMDLREEGD-----	61		
Db	2	GNIPKAKTPIRLCILENDWQCDTQTLRKRRIFFCSTAMPQYPLQGRETWLPGESINYNI	61		
QY	62	-----EETTVDPHIQCGDCDPOGLRNSQFCQLRIHQGLIFYEKLGLSDIFTG	111		
Db	62	ILQLDLFCRKEGKWSVEVPVQTF-----FSLRNSQLC-----KKCGL-CPTG	103		
QY	112	EPSLLP-----DSPVAQLHASLGLLSQLQPE-----GHHWETQOIPSL	153		
Db	104	SPQSPPPYPVPPPTPSSTNKKDP-----LTQTVQKEIDKGVNNEPKSANIPRLC	153		
QY	152	PSQ 154			
Db	154	PLQ 156			
RESULT 10					
Q9WVQ8	PRELIMINARY; PRT; 210 AA.				
ID	Q9WVQ8				
AC	Q9WVQ8;				
DT	01-NOV-1999 (TReMBLrel. 12, Created)				
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)				
DT	01-OCT-2001 (TReMBLrel. 18, Last annotation update)				
DE	IL-6 (fragment).				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
OC	Mesocricetus				
OX	NCBI_TaxID=10036;				

```
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA78766.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER
SQ SEQUENCE 210 AA; 24060 MW; BD9319AFBB913AB3 CRC64;

Query Match      8.4%; Score 84.5; DB 11; Length 210;
Best Local Similarity 24.7%; Pred. No. 0.93;
Matches 44; Conservative 24; Mismatches 69; Indels 41; Gaps 8;

QY 28 PAWTOCQQ-----LSQKLCITLAWSAHPLVGHMDLREEGE---ETTNDVPH 70
DB 42 PVTTSQQVGLVTVLREIYELRKELC-----NNNP--GCM-----NDYVLLENLPLV 91
QY 71 IQCGGCDPQGLRDSNQFLQRIHQGLIFYEKLIGSDIFTGEPSSLPSVAOLHASLLG 130
DB 92 IQINDGCLQTGY--NWEICLLKITSGLLDYQIYL--EFVTNNVDNKKKARVITQSTIKT 147
QY 131 LSQLLOPEGHWHWETQIIPS-----LSPSQPWORLLRLRSLQAFVAVAAAR 178
DB 148 LSQIFQKQVGGPKDQIVTSPSTSKAILMEKLESQKQWPKTKILKILKALEEFLEVIMR 205

RESULT 11
Q9P245 PRELIMINARY; PRT; 137 AA.
AC Q9P245;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE gag polyprotein (fragment).
OS multiple sclerosis associated retrovirus element.
OC Viruses; Retroviridae.
OX NCBI_TaxID=89382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99335590; PubMed=10405350;
RA Komurian-Pradel F., Paranhos-Baccala G., Bedin F., Ounanian-Paraz A.,
RA Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,
RA Perron H.;
RT "Molecular cloning and characterization of MSRV-related sequences
associated with retrovirus-like particles.";
RL Virology 260:1-9(1999).
DR EMBL; AF123880; AAD48374.1; -.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 137 AA; 15662 MW; 8F43D05636CD958E CRC64;

Query Match      8.3%; Score 83; DB 15; Length 137;
Best Local Similarity 28.6%; Pred. No. 0.8;
Matches 28; Conservative 7; Mismatches 31; Indels 32; Gaps 5;

QY 19 GRAVPGGSPA-----WTQC--QQLSQK-----LCTLAWSAHPLVGHMDLREEGD----- 61
DB 2 GNVPEAKMPLERILENNQDQDTQLRKREIFTCSTAWQYPLQGRWLPQGSINVINI 61
QY 62 -----ETTNDVPHIQCGDCDQGLRDSNQFC 89
DB 62 ILQLDLCKRKQKWSVEPVYQTF-----FSLRDSNQLC 94

RESULT 12
Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
(Delphinapterus leucas) interleukin 6.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match      8.2%; Score 82; DB 6; Length 208;
Best Local Similarity 23.9%; Pred. No. 1.7;
Matches 32; Conservative 23; Mismatches 59; Indels 20; Gaps 4;

QY 58 EEDEETTNDVPHIQCGDCDQGLRDSNQFLQRIHQGLIFYEKLIG--SDIFTGEPSSL 115
DB 77 KEALAEENLNLPKMAEKDQCFQSGF--NOETCLMRITITGLLEYQIYDLQNEYEGD--- 131
QY 116 LPDSPVAOLHASLLGLSLOLQPEGHWHWETQIIPS-----LSPSQPWORLLRLR 164
DB 132 --KGSIEAVQISIKALQILKQKVNPDVTPDPTTNASLMNNLQSONDDMRNTKIIL 189
QY 165 ILRLSLQAFVAVAAAR 178
DB 190 ILRLSLENLQFSLR 203

RESULT 13
Q923K0 PRELIMINARY; PRT; 858 AA.
AC Q923K0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Sweet taste receptor TIR3.
GN TASIR3 OR SAC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWR/J;
RA Nelson G., Hoon M.A., Chandrashekar J., Zhang Y., Ryba N.J.P.,
RA Zuker C.S.;
RT "Mammalian Sweet Taste Receptors.";
RL Cell 0:0-0(2001).
DR EMBL; AY032621; AAK51602.1; -.
DR MGD; MGI:1933547; Tas1r3.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
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DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; UNKNOWN\_1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW Receptor.  
SQ SEQUENCE 858 AA; 94530 MW; 686A7E524267796A CRC64;

Query Match 8.2%; Score 82; DB 11; Length 858;  
Best Local Similarity 27.4%; Pred. No. 8.9;  
Matches 51; Conservative 10; Mismatches 65; Indels 60; Gaps 11;  
QY 3 GSRAVMLLLPWTAGRAVPGGSSPAWTCQOOLSKLCTLAWSAHLVGHMDLREEGDE 62  
DB 570 GEPWLSLLL-----LCIVLGALAAALGLSVH-----HW----- 599  
QY 63 ETNDVPHIQCGCDPQGLRDNISQFCLRIHQGLIFYEKLIGSDIFTGEP---SLLPDS 119  
DB 600 -----DSPVQASGG-----SQCFGLICGLFCLSVLL-----FPGRPSSASCLAQQ 642  
QY 120 PVAQLHASILG-LSQLLPQEGHHWETQIPSLSPSPQWORLLLRKILRSLOAFVAVAAR 178  
DB 643 PMA--HLPLTGLCLSTFLQAAETFVESELP-LS----WANWLCYS--LRGLWAWLVLSA 693  
QY 179 VFAHGA 184  
DB 694 TFVEAA 699

## RESULT 14

Q912L3 PRELIMINARY; PRT; 212 AA.  
AC Q912L3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Interleukin 6.  
OS Sigmomon hispidus (Hispid cotton rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
OC Sigmodon.  
OX NCBI\_TaxID=42415;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PERIPHERAL BLOOD;  
RA Blanco J.C., Pletneva L.M., Prince G.A.;  
RT "Sigmomon hispidus cytokines, chemokines and interferons."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF421389; AAL18819.1; -  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR InterPro; IPR003574; Interleukin\_6.  
DR InterPro; IPR003580; Protachykinin.  
DR Pfam; PF00489; IL6; 1.  
DR ProDom; PD004356; Interleukin\_6; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00254; INTERLEUKIN\_6; UNKNOWN\_1.  
SQ SEQUENCE 212 AA; 24406 MW; 97E1C47CED080D5D CRC64;

Query Match 8.1%; Score 81.5; DB 11; Length 212;  
Best Local Similarity 23.8%; Pred. No. 1.9;  
Matches 38; Conservative 25; Mismatches 64; Indels 33; Gaps 7;

QY 35 QLSQKCLTANSAHPLVGHMDLREEGD--EETNDVPHIQCGCDPQGL-RDINSQFCLQ 91  
DB 65 QMSKELCN-----NNPCMTWDDALSENNDLPVIERNDGCFQTGYDREN---CLL 112  
QY 92 RIHQGLIFYE---KLIGSDIFTGPPSLPDSFVAQLHASLLGLSOLLQPEGHHWETQIIP 148  
DB 113 KITSGLLDYQIYLEFLKNNVDNK-----KERARVQNSTRKALNQILKQEVKDPCKTATP 167  
QY 149 S-----LSPSQPWORLLLRKILRSLOAFVAVAAR 178  
DB 143 SPTSKVLLMEKLESQKDWPRTKTIQLILKALEEFLKTIIMR 207

## RESULT 15

Q95K25 PRELIMINARY; PRT; 540 AA.  
AC Q95K25;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Hypothetical 59.3 kDa protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Hashimoto K., Osada N., Kusuda J., Tanuma R., Hirai M.,  
RT Terao K., Sugano S.; full-length cDNA clones from macaque testis cDNA  
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA  
RT libraries."  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB070002; BAB62947.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 540 AA; 59344 MW; A3ADF80610954982 CRC64;

Query Match 8.1%; Score 81.5; DB 6; Length 540;  
Best Local Similarity 28.3%; Pred. No. 5.8;  
Matches 36; Conservative 17; Mismatches 43; Indels 31; Gaps 6;

QY 54 MDLREEGDEETNDVPHIQCGCDPQ-GLRDN---SQFCLRIHQGLIFYEKLIGSDIF 109  
DB 415 VDMROEQLOGFNQVGERRAQAGFAPQTGARPSETFARFCKSQ-----DSALGST-- 464  
QY 110 TGEPSILLPDSFVAQLHASLL-----GLSOLLQPEGHHWETQIIPSLSP-----SQ 154  
DB 465 --DPAVEPTPSLDVLAQPLEASSPAEGLTQPLQGGTPHNEPCQLPSPSPGLSEVLQAQ 522  
QY 155 PWQRLLL 161  
DB 523 PQGALAL 529

Search completed: November 20, 2002, 11:54:24  
Job time : 28.0182 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:39 : Search time 32.4 Seconds  
(without alignments)  
777.295 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRVAVMLLLPWTAGR.....QAFVAVARVFAHGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1004	100.0	189	20	AA1980
2	1004	100.0	189	20	AA1981
3	1004	100.0	189	21	AA1982
4	1004	100.0	189	22	AA1983
5	1000	99.6	189	21	AA1984
6	1000	99.6	189	21	AA1985
7	1000	99.6	189	22	AA1986
8	1000	99.6	189	22	AA1987
9	718.5	71.6	196	20	AA1988
10	718.5	71.6	196	20	AA1989

11	718.5	71.6	196	21	AA1990
12	718.5	71.6	196	22	AA1991
13	463	46.1	102	20	AA1992
14	463	46.1	102	20	AA1993
15	463	46.1	102	21	AA1994
16	107	10.7	175	21	AA1995
17	105	10.5	175	21	AA1996
18	103	10.3	175	21	AA1997
19	103	10.3	175	21	AA1998
20	102	10.2	174	21	AA1999
21	102	10.2	174	23	AA2000
22	102	10.2	175	21	AA2001
23	102	10.2	307	16	AA2002
24	102	10.2	307	16	AA2003
25	102	10.2	307	16	AA2004
26	102	10.2	307	16	AA2005
27	102	10.2	307	21	AA2006
28	102	10.2	307	21	AA2007
29	102	10.2	307	21	AA2008
30	102	10.2	307	21	AA2009
31	102	10.2	307	22	AA2010
32	102	10.2	307	22	AA2011
33	102	10.2	307	22	AA2012
34	102	10.2	307	22	AA2013
35	102	10.2	307	22	AA2014
36	102	10.2	307	22	AA2015
37	102	10.2	307	22	AA2016
38	102	10.2	307	22	AA2017
39	102	10.2	307	22	AA2018
40	102	10.2	307	22	AA2019
41	102	10.2	307	22	AA2020
42	102	10.2	307	22	AA2021
43	102	10.2	307	22	AA2022
44	102	10.2	307	22	AA2023
45	102	10.2	307	22	AA2024

#### ALIGNMENTS

##### RESULT 1

```

AA1980
ID AA1980 standard; Protein; 189 AA.
XX AA1980
AC AA1980
DT 04-NOV-1999 (first entry)
DE Human interleukin B30.
DE DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
DE interleukin B30; DSR1; IL-B30; cytokine receptor; diagnosis;
DE inflammatory disorder; inflammatory response; innate immunity;
DE morphogenic development; immunological disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein /label= signal
XX /label= IL-B30
XX WO9940195-A1.
XX PD 12-AUG-1999.
XX PF 05-FEB-1999; 99WO-US02600.
XX PR 13-MAY-1998; 98US-0078194.
XX PR 06-FEB-1998; 98US-0073941.
XX (SCHE ) SCHERING CORP.

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XX PI Kastelein RA, Mattson JD, McClanahan TK;  
 XX DR WPI; 1999-527306/44.  
 XX DR N-PSDB; AAZ08865.  
 XX PT New receptor subunits useful in the treatment inflammatory disorders  
 XX PS Claim 2; Page 26-27; 133pp; English.  
 XX CC The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DSRS1) protein, which together encode a new mammalian  
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
 CC proteins, or DSRS1 and IL-B30 proteins. (I) comprising DSRS1 and DCRS1  
 CC is useful for screening for ligands (i.e. agonists/antagonists) from  
 CC a library of compounds, which are useful for modulating the physiology  
 CC or development of a cell or tissue culture e.g. inflammatory responses,  
 CC innate immunity and/or morphogenic development. (R), antibodies and  
 CC ligands are useful for treatment of conditions, especially immunological  
 CC disorders, associated with conditions exhibiting abnormal expression of  
 CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
 CC and the subunits DSRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids  
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
 CC variants from other individuals or species. The present sequence  
 CC represents the specifically claimed human IL-B30, for use in the  
 CC composition of the present invention.  
 XX CC Sequence 189 AA;  
 XX SQ

Query Match 100.0%; Score 1004; DB 20; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-97;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
 Db 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120  
 Db 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180  
 Db 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180

Qy 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189

RESULT 2  
 AA95002  
 XX ID AA95002 standard; Protein; 189 AA.  
 XX AC AA95002;  
 XX CC  
 XX DT 21-MAY-1999 (first entry)  
 XX DE Human interleukin-B30 (IL-B30) polypeptide.  
 XX DE Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
 KW inflammatory condition; drug screening; human.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /note= "signal peptide"  
 FT 22..189  
 FT Protein /note= "mature protein"  
 XX

PN WO9905280-A1.  
 XX PD 04-FEB-1999.  
 XX PF 24-JUL-1998; 98WO-US15423.  
 XX PR 25-JUL-1997; 97US-0900905.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Bazan JF;  
 XX DR WPI; 1999-1429335/12.  
 XX DR N-PSDB; AAX17786.  
 XX PT Newly isolated or recombinant polynucleotide encoding mammalian  
 PT cytokine interleukin-B30 (IL-B30), including fragments - useful for  
 PT regulating activation, development, differentiation and function of  
 PT various cell types, and for diagnosing and treating conditions  
 PT associated with IL-B30  
 XX PS Claim 2; Page 8-9; 83pp; English.  
 XX CC This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.  
 CC Host cells containing a vector comprising the IL-B30 nucleic acid are  
 CC used for the recombinant production of the protein. The polynucleotides  
 CC are useful for diagnosis of IL-B30 mediated conditions, and forensic  
 CC science (e.g. to distinguish rodent from human, or as a marker to  
 CC distinguish between different cells exhibiting differential expression or  
 CC modification patterns). The IL-B30 (including fragments), together with  
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They  
 CC are also used for treating conditions associated with abnormal physiology  
 CC or development, including inflammatory conditions. The polypeptide  
 CC cytokine should mediate cytokine synthesis and proliferation in cells.  
 CC IL-B30 is useful for drug screening to identify compounds having binding  
 CC affinity to IL-B30.  
 XX CC Sequence 189 AA;  
 XX SQ

Query Match 100.0%; Score 1004; DB 20; Length 189;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-97;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
 Db 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120  
 Db 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180  
 Db 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180

Qy 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189

RESULT 3  
 AAB01981  
 XX ID AAB01981 standard; Protein; 189 AA.  
 XX AC AAB01981;  
 XX CC  
 XX DT 27-SEP-2000 (first entry)  
 XX DE Human interleukin-B30 (IL-B30).  
 XX DE Interleukin-B30; IL-B30; human; cytokine; cellular signalling;  
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
 KW granulocyte colony stimulating factor; Immune disorder;  
 XX

inflammatory disease; autoimmune disease; antigen; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..21

XX FT Protein /note= "Signal peptide"

XX FT Protein 22..189

XX FT Protein /note= "Mature human IL-B30"

XX PN US060284-A.

XX PD 09-MAY-2000.

XX PF 24-JUL-1998; 98US-0122443.

XX PR 25-JUL-1997; 97US-0053765.

XX PA (SCHE ) SCHERING CORP.

XX PI Bazan JF;

XX DR WPI; 2000-364420/31.

XX DR N-PSDB; AAA52577.

XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30

XX PT useful as probes or primers for diagnosing immune disorders including

XX PT autoimmune or chronic inflammatory conditions

XX PS Claim 1; Column 5-8; 32pp; English.

XX CC This sequence represents human interleukin-B30 (IL-B30). IL-B30

XX CC is a novel cytokine, exhibiting significant homology to IL-6 and

XX CC G-CSF (granulocyte colony stimulating factor). Cytokines play a critical

XX CC role in signalling between immune or other cells during an immune

XX CC response. The precise role of IL-B30 is not yet known - it is likely to

XX CC have either a stimulatory or an inhibitory effect on haematopoietic cells

XX CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.

XX CC Alternatively, it may affect vascular physiology or development, or have

XX CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and

XX CC antagonists are useful in the diagnosis and treatment of disorders

XX CC associated with abnormal expression or activity of IL-B30 e.g.,

XX CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are

XX CC useful for recombinant expression of IL-B30 in a host cell, and as a

XX CC source of probes and primers. The IL-B30 probes and primers can be used

XX CC to detect levels of IL-B30 expression in samples from patients suspected

XX CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may

XX CC also be used to identify homologous genes in other species. IL-B30

XX CC protein or its fragments are useful as antigens for raising antibodies to

XX CC various linear and conformational epitopes. Such antibodies may be used

XX CC to detect levels of IL-B30 protein in a sample.

XX SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 21; Length 189;

Best Local Similarity 100.0%; Pred. No. 3.2e-97;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCCQLSOKLCTLAWSAHLVGHMDLREG 60

DB 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCCQLSOKLCTLAWSAHLVGHMDLREG 60

QY 61 DEETNDVPHICGGCDPQGLRDNRSQFCLQRIHQGLLFYFKLGSDFTGEPSSLDPSP 120

DB 61 DEETNDVPHICGGCDPQGLRDNRSQFCLQRIHQGLLFYFKLGSDFTGEPSSLDPSP 120

QY 121 VAQLHASLGLSOLLQPEGHWHWETQIQIPSLSPSQWRLFRKILRSLOAFVAAARVF 180

DB 121 VAQLHASLGLSOLLQPEGHWHWETQIQIPSLSPSQWRLFRKILRSLOAFVAAARVF 180

QY 181 AHGAATLSP 189

DB 181 AHGAATLSP 189

## RESULT 4

AAB47120

ID AAB47120 standard; Protein; 189 AA.

XX AC AAB47120;

XX DT 04-JUN-2001 (first entry)

XX DE Human IL-B30.

XX KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;

XX KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;

XX KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;

XX KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;

XX KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;

XX KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;

XX KW Castleman's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..21

XX FT Protein /note= "Signal peptide"

XX FT Protein 22..189

XX FT Protein /note= "Mature protein"

XX PN WO200118051-A2.

XX PD 15-MAR-2001.

XX PF 08-SEP-2000; 2000WO-US24686.

XX PR 09-SEP-1999; 99US-0393090.

XX PR 10-NOV-1999; 99US-0164616.

XX PA (SCHE ) SCHERING CORP.

XX PI Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;

XX PI Wiekowski MT, Lira SA, Narula SK;

XX PN WPI; 2001-244560/25.

XX DR N-PSDB; AAC85540.

XX PT Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its

XX PT segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,

XX PT atherosclerosis, multiple sclerosis, vasculitis and tumour

XX PS Disclosure; Page 10-11; 69pp; English.

XX CC This sequence shows human interleukin-B30. Fragments of this protein

XX CC may be used in the composition of the invention. The composition

XX CC comprises a substantially pure polypeptide comprising a number of

XX CC distinct segments of at least 7 contiguous amino acids from IL-12 p40

XX CC and/or IL-B30, and a substantially pure polypeptide comprising a

XX CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or

XX CC IL-B30. The composition is useful for modulating physiology or

XX CC development of a cell or tissue in a host organism, resulting in an

XX CC increased or decreased production of Interferon-gamma (IFNgamma), an

XX CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,

XX CC anti-viral effect or antagonized allergic effect, and amelioration

XX CC of an autoimmune condition or a chronic inflammatory condition.

XX CC IL-B30 or its agonist is useful inducing the proliferation of memory

XX CC T-cells. An agonist or antagonist of IL-B30 protein is useful for

XX CC modulating the trafficking or activation of a leukocyte in an animal

XX CC experiencing science or symptoms of autoimmunity, an inflammatory

XX CC condition, tissue specific autoimmunity, degenerative autoimmunity,

XX CC rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple

XX CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a

XX CC transplant, spinal injury, stroke, neurodegeneration, an infectious

XX CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's

XX CC disease, postmenopausal osteoporosis or IL-6-associated diseases.

```
CC IL-12 p40/IL-B30 is useful as an immunogen for the production a
CC antisera or antibodies specific for binding.
XX
SQ Sequence 189 AA;
Query Match 100.0%; Score 1004; DB 22; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.2e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVAVMLLLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Db 1 MLGSRVAVMLLLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRHOGILFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRHOGILFYEKLLGSDIFTGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSOLLQPEGHWHWTQIIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
Db 121 VAQLHASLLGLSOLLQPEGHWHWTQIIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189
RESULT 5
AAAY94966
ID AAAY94966 standard; Protein; 189 AA.
XX
AC AAAY94966;
XX
DT 16-JUN-2000 (first entry)
DE Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138.
KW Human; secreted protein; immunestimulant; immunosuppressant; virucide;
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
KW connective tissue disease; multiple sclerosis; erythematosis;
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
KW insulin dependent diabetes mellitus; graft-versus-host-disease;
KW autoimmune inflammatory eye disease; allergy.
XX
OS Homo sapiens.
XX
PN WO200009552-A1.
XX
PD 24-FEB-2000.
XX
PF 13-AUG-1999; 99WO-US18298.
XX
PR 14-AUG-1998; 98US-0096622.
XX
PR 17-AUG-1998; 98US-0096815.
XX
PR 04-SEP-1998; 98US-0095229.
XX
PR 23-OCT-1998; 98US-0105368.
XX
PR 08-JAN-1999; 99US-0115234.
XX
PR 12-FEB-1999; 99US-0119931.
XX
PR 18-FEB-1999; 99US-0120575.
XX
PR 30-APR-1999; 99US-0132020.
XX
PR 11-AUG-1999; 99US-0096622.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;
PI Wong GG, Clark HF, Fachtel K;
XX
DR WPI; 2000-205979/18.
XX
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```
PT New polynucleotides encoding secreted proteins, which may have e.g.
PT nutritional, chemokine, immune stimulating or suppressing,
PT hematopoiesis regulating, tissue growth, activin/inhibin
PT antinflammatory or tumor inhibition activity
XX
Claim 147; Page 597; 64lpp; English.
XX
AAAL6618 to AAAL6697 encode the human secreted proteins given in
CC
CC AAAY94898 to AAAY94980, isolated from human adult brain, adult thyroid,
CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,
CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
CC and adult bladder, cDNA libraries. The polynucleotides and proteins are
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans
CC and animals. The polynucleotides can be used as markers for tissues in
CC which the protein is preferentially expressed, as molecular weight
CC markers on Southern gels, and as chromosome markers or tags to identify
CC chromosomes or to map gene positions. The proteins can be used in the
CC treatment of immune deficiencies and disorders, such as severe combined
CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
CC infections. These infections include human immunodeficiency virus (HIV),
CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
CC candidiasis. The proteins can be used to treat autoimmune disorders such
CC as connective tissue disease, multiple sclerosis, systemic lupus
CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependant
CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
CC autoimmune inflammatory eye disease. The proteins can also be used to
CC treat allergic conditions, such as asthma. AAAL6698 to AAAL6774 represent
CC probes for the human secreted proteins from the present invention.
XX
SQ Sequence 189 AA;
Query Match 99.6%; Score 1000; DB 21; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MLGSRVAVMLLLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Db 1 MLGSRVAVMLLLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRHOGILFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRHOGILFYEKLLGSDIFTGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSOLLQPEGHWHWTQIIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
Db 121 VAQLHASLLGLSOLLQPEGHWHWTQIIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189
RESULT 6
AAAY54606
ID AAAY54606 standard; Protein; 189 AA.
XX
AC AAAY54606;
XX
DT 01-FEB-2000 (first entry)
XX
DE SGRF protein sequence.
XX
KW SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
KW immune system; haematopoietic system; therapy.
XX
OS Homo sapiens.
XX
PN WO9954357-A1.
XX
PD 28-OCT-1999.
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XX PF 14-APR-1999; 99WO-JP01997.
XX PR 14-APR-1998; 98JP-0121805.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Hirata Y;
XX DR WPI: 2000-013230/01.
XX DR N-PSDB; AAZ37262, AAZ37263.
XX PR Novel cytokine-like protein, with activity of supporting proliferation
PT of myeloid cells, useful in treating abnormality of cell proliferation
PT in immune and haematopoiesis systems
XX PS Claim 1; Fig 1; 69pp; Japanese.
XX CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.
XX SQ Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 21; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLTCTLAWSAHLVGHMDLREG 60
DB 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLTCTLAWSAHLVGHMDLREG 60

QY 61 DEETNDVPHIQCGDGDQGLRDNQSQCFLQRIHQGLIFVEKLLGSDIFTGEPFLLPSP 120
DB 61 DEETNDVPHIQCGDGDQGLRDNQSQCFLQRIHQGLIFVEKLLGSDIFTGEPFLLPSP 120

QY 121 VAQLHASLLGLSQLLQPEGHWHWTQIIPSLSPSPQWRLLRKLRSLOAFVAAVAF 180
DB 121 VQQLHASLLGLSQLLQPEGHWHWTQIIPSLSPSPQWRLLRKLRSLOAFVAAVAF 180

QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 7
AAU12287
ID AAU12287 standard; Protein; 189 AA.
XX AC AAU12287;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO5798 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US32678.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 01-DEC-1999; 99WO-US28634.
XX PR 02-DEC-1999; 99WO-US28551.

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PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX

(GETH ) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2001-408281/43.
DR N-PSDB; AA521359.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 232; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 189 AA;
SQ

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Query Match 99.6%; Score 1000; DB 22; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLTCTLAWSAHLVGHMDLREG 60
DB 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLTCTLAWSAHLVGHMDLREG 60
QY 61 DEETNDVPHIQCGDGDQGLRDNQSQCFLQRIHQGLIFVEKLLGSDIFTGEPFLLPSP 120

```

Db 61 DEETNDVPHIOGDCDPOGLRDNQSFCLQRHOGCLIFYEKLLGSDIFTGEPSSLDPSP 120  
 QY 121 VAQLHASLLGSLQLLOPEGHWHWTQIPLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180  
 Db 121 VGQLHASLLGSLQLLOPEGHWHWTQIPLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180  
 QY 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189  
 RESULT 8  
 AAB48070  
 ID AAB48070 standard; protein; 189 AA.  
 XX  
 AC AAB48070;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human extracellular signaling molecule (EXCS) (ID 2933038CD1).  
 XX  
 KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;  
 KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;  
 KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;  
 KW antinfertility; cerebroprotective; nootropic; antiulcer; antifungal;  
 KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;  
 KW keratolytic; protozoacide; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200070049-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 19-MAY-2000; 2000WO-US13975.  
 XX  
 PR 19-MAY-1999; 99US-0134949.  
 PR 15-JUL-1999; 99US-0144270.  
 PR 30-JUL-1999; 99US-0146700.  
 PR 04-OCT-1999; 99US-0157508.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;  
 PI Azimzai Y, Lu DAM, Patterson C;  
 XX  
 DR WPI; 2001-025021/03.  
 DR N-PSDB; AAC84306.  
 XX  
 XX New human extracellular signaling nucleic acids and polypeptides useful  
 PT for diagnosing, treating and preventing infections and  
 PT gastrointestinal, neurological, reproductive, and  
 PT autoimmune/inflammatory disorders -  
 XX  
 PS Claim 1; Page 92; 114pp; English.  
 XX  
 XX The invention provides human extracellular signaling molecules (EXCS)  
 CC and polynucleotides which identify and encode EXCS. EXCS can be  
 CC expressed by standard recombinant methodology. The amino acid and nucleic  
 CC acid sequences of EXCS are useful for diagnosing, treating and  
 CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,  
 CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular  
 CC disease, stroke), reproductive (infertility, ovulatory defects,  
 CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired  
 CC immunodeficiency syndrome (AIDS), Addison's disease), and cell  
 CC proliferative disorders including cancers (of the breast, adrenal gland,  
 CC bone). They may also be used to treat fatal familial insomnia,  
 CC nutritional and metabolic diseases of the nervous system, myopathies,  
 CC mental disorders (anxiety, schizophrenia, mood), as well as infections  
 CC caused by parasites (malaria, leishmaniasis, trypanosoma), viral  
 CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,  
 CC staphylococcus, bacillus), and fungal (aspergillus, blastomyces,

CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,  
 CC agonists, pharmaceutical compositions, and antibodies may also be used  
 CC for treating or preventing disorders associated with increased or  
 CC decreased expression or activity of EXCS. EXCS polynucleotides may also  
 CC be used to detect and quantify gene expression in biopsied tissues in  
 CC which expression of EXCS may be correlated with the disease, to determine  
 CC presence or excess expression of EXCS, to monitor regulation of EXCS  
 CC levels during therapeutic intervention, to detect the presence of  
 CC associated disorders, as targets in microarray, to generate hybridization  
 CC probes, and to detect differences in gene sequences among normal, carrier  
 CC or affected individuals. Antibodies may also be used in diagnosing  
 CC disorders, in monitoring patients being treated with EXCS agonists,  
 CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS  
 CC of the invention.  
 XX  
 SQ Sequence 189 AA;  
 XX  
 Query Match 99.6%; Score 1000; DB 22; Length 189;  
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;  
 Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps  
 QY 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTQCQQLSQKLCCTLAWSAHLVGHMDLREEG 60  
 Db 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTQCQQLSQKLCCTLAWSAHLVGHMDLREEG 60  
 QY 61 DEETNDVPHIOGDCDPOGLRDNQSFCLQRHOGCLIFYEKLLGSDIFTGEPSSLDPSP 120  
 Db 61 DEETNDVPHIOGDCDPOGLRDNQSFCLQRHOGCLIFYEKLLGSDIFTGEPSSLDPSP 120  
 QY 121 VAQLHASLLGSLQLLOPEGHWHWTQIPLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180  
 Db 121 VGQLHASLLGSLQLLOPEGHWHWTQIPLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180  
 QY 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189  
 RESULT 9  
 AAY29784  
 ID AAY29784 standard; Protein; 196 AA.  
 XX  
 AC AAY29784;  
 XX  
 DT 04-NOV-1999 (first entry)  
 XX  
 DE Mouse interleukin B30.  
 XX  
 KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW interleukin B30; DSR51; DCR51; IL-B30; cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenic development; immunological disorder.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= signal  
 FT 22..196  
 FT /label= IL-B30  
 XX  
 PN W09940195-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 05-FEB-1999; 99WO-US02600.  
 XX  
 PR 13-MAY-1998; 98US-0078194.  
 PR 06-FEB-1998; 98US-0073941.  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Kastelein RA, Mattson JD, McClanahan TK;

XX WPI; 1999-527306/44.  
 DR N-PSDB; AAZ08866.  
 XX  
 PT New receptor subunits useful in the treatment inflammatory disorders  
 XX  
 PS Claim 2; Page 27-28; 133pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DCRS1) protein, which together encode a new mammalian  
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
 CC proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1  
 CC is useful for screening for ligands (i.e. agonists/antagonists) from  
 CC a library of compounds, which are useful for modulating the physiology  
 CC or development of a cell or tissue culture e.g. inflammatory responses,  
 CC innate immunity and/or morphogenic development. (R), antibodies and  
 CC ligands are useful for treatment of conditions, especially immunological  
 CC disorders, associated with conditions exhibiting abnormal expression of  
 CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
 CC and the subunits DCRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids  
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
 CC variants from other individuals or species. The present sequence  
 CC represents the specifically claimed mouse IL-B30, for use in the  
 CC composition of the present invention.  
 XX  
 SQ Sequence 196 AA;  
 Query Match 71.6%; Score 718.5; DB 20; Length 196;  
 Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLCGRVAMLLLLPWTAGRAVPGCGSSPAWTCQQLSQKCLTSAHPLVGHMD-LREE 59  
 DB 1 MLCRAVIMLWLPWVTQGLAVPRSSPDWAQCCQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 QY 60 GDEETNDVPHIQCGDCDQGLRDNSQFCQLRIHQGLIFYEKLGLSGDIFTGEPSPLLPDS 119  
 DB 61 EDEETKNVPRIQCEDCDQGLKDNSQFCQLRIHQGLAFYKHLSDIFKGEPAALLPDS 120  
 QY 120 PVAQLHASLLGLSOLLOPEGHWHWETQIIPSLSPSPQWRLRLRFLKILRSLOAFVAVARV 179  
 DB 121 PMEQLHTSLGLSOLLOPEDHPRETQOMPSPSSSQWQORPLRLSKILRSLOAFVAVARV 180  
 QY 180 FAHGAATIS 188  
 DB 181 FAHGAATLT 189  
 RESULT 10  
 ID AAW95003 standard; Protein; 196 AA.  
 AC AAW95003;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Mouse interleukin-B30 (IL-B30) polypeptide.  
 XX  
 KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
 KW inflammatory condition; drug screening; mouse.  
 OS  
 XX Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /note= "signal peptide"  
 FT Protein 22..196  
 FT /note= "mature protein"  
 XX  
 PN W09905280-A1.  
 XX

PD 04-FEB-1999.  
 XX  
 PF 24-JUL-1998; 98WO-US15423.  
 XX  
 PR 25-JUL-1997; 97US-0900905.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 XX Bazan JF;  
 PI  
 XX WPI; 1999-142935/12.  
 DR N-PSDB; AAX17787.  
 XX  
 PT Newly isolated or recombinant polynucleotide encoding mammalian  
 PT cytokine interleukin-B30 (IL-B30), including fragments - useful for  
 PT regulating activation, development, differentiation and function of  
 PT various cell types, and for diagnosing and treating conditions  
 PT associated with IL-B30  
 XX  
 PS Claim 2; Page 9-10; 83pp; English.  
 XX  
 CC This represents a mouse cytokine interleukin-B30 (IL-B30) polypeptide.  
 CC Host cells containing a vector comprising the IL-B30 nucleic acid are  
 CC used for the recombinant production of the protein. The polynucleotides  
 CC are useful for diagnosis of IL-B30 mediated conditions, and forensic  
 CC science (e.g. to distinguish rodent from human, or as a marker to  
 CC distinguish between different cells exhibiting differential expression or  
 CC modification patterns). The IL-B30 (including fragments), together with  
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They  
 CC are also used for treating conditions associated with abnormal physiology  
 CC or development, including inflammatory conditions. The polypeptide  
 CC cytokine should mediate cytokine synthesis and proliferation in cells.  
 CC IL-B30 is useful for drug screening to identify compounds having binding  
 CC affinity to IL-B30.  
 XX  
 SQ Sequence 196 AA;  
 Query Match 71.6%; Score 718.5; DB 20; Length 196;  
 Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLCGRVAMLLLLPWTAGRAVPGCGSSPAWTCQQLSQKCLTSAHPLVGHMD-LREE 59  
 DB 1 MLCRAVIMLWLPWVTQGLAVPRSSPDWAQCCQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 QY 60 GDEETNDVPHIQCGDCDQGLRDNSQFCQLRIHQGLIFYEKLGLSGDIFTGEPSPLLPDS 119  
 DB 61 EDEETKNVPRIQCEDCDQGLKDNSQFCQLRIHQGLAFYKHLSDIFKGEPAALLPDS 120  
 QY 120 PVAQLHASLLGLSOLLOPEGHWHWETQIIPSLSPSPQWRLRLRFLKILRSLOAFVAVARV 179  
 DB 121 PMEQLHTSLGLSOLLOPEDHPRETQOMPSPSSSQWQORPLRLSKILRSLOAFVAVARV 180  
 QY 180 FAHGAATIS 188  
 DB 181 FAHGAATLT 189  
 RESULT 11  
 ID AAB01982  
 XX  
 XX AAB01982 standard; Protein; 196 AA.  
 AC AAB01982;  
 XX  
 DT 27-SEP-2000 (first entry)  
 XX  
 DE Murine interleukin-B30 (IL-B30).  
 XX  
 KW Interleukin-B30; IL-B30; murine; mouse; cytokine; cellular signalling;  
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
 KW granulocyte colony stimulating factor; immune disorder;  
 KW inflammatory disease; autoimmune disease; antigen; antibody.  
 XX

OS Mus sp.  
XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..196  
FT /note= "Mature murine IL-B30"  
XX  
XX US6060284-A.  
PN  
XX  
XX 09-MAY-2000.  
PD  
XX  
XX 24-JUL-1998; 98US-0122443.  
PF  
XX  
XX 25-JUL-1997; 97US-0053765.  
PR  
XX (SCHE ) SCHERING CORP.  
PA  
XX  
XX Bazan JF;  
FI  
XX  
XX WPI: 2000-364420/31.  
DR N-PSDB; AAA52578.  
XX  
XX Novel recombinant DNA encoding cytokines especially interleukin-B30  
PT useful as probes or primers for diagnosing immune disorders including  
FT autoimmune or chronic inflammatory conditions -  
XX  
XX Claim 1; Column 7-10; 32pp; English.  
PS  
XX  
XX This sequence represents murine interleukin-B30 (IL-B30). IL-B30  
CC is a novel cytokine, exhibiting significant homology to IL-6 and  
CC G-CSF (granulocyte colony stimulating factor). Cytokines play a critical  
CC role in signalling between immune or other cells during an immune  
CC response. The precise role of IL-B30 is not yet known - it is likely to  
CC have either a stimulatory or an inhibitory effect on haematopoietic cells  
CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.  
CC Alternatively, it may affect vascular physiology or development, or have  
CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and  
CC antagonists are useful in the diagnosis and treatment of disorders  
CC associated with abnormal expression or activity of IL-B30 e.g.,  
CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are  
CC useful for recombinant expression of IL-B30 in a host cell, and as a  
CC source of probes and primers. The IL-B30 probes and primers can be used  
CC to detect levels of IL-B30 expression in samples from patients suspected  
CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may  
CC also be used to identify homologous genes in other species. IL-B30  
CC protein or its fragments are useful as antigens for raising antibodies to  
CC various linear and conformational epitopes. Such antibodies may be used  
CC to detect levels of IL-B30 protein in a sample.  
XX  
XX Sequence 196 AA;  
SQ  
Query Match 71.6%; Score 718.5; DB 21; Length 196;  
Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLGSRVALLLLPWTAGRAVPGCGSSPAWTCQOLSKQKCTLAWSAHLVGHMD-LREE 59  
DB 1 MUDCRVIMLLPWTGGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHWNLLREE 60  
QY 60 GDEETNDVPHITQCGDGPQGLRDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLPDS 119  
DB 61 EDEETKNVPRIQCEGDCPQGLKDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLPDS 120  
QY 120 PVAQLHASLLGSLQQLPEGHWHETQITPSLSPSQWQRLRLRPKILRSLOAFVAARV 179  
DB 121 PNEOLHTSLGSLQQLPEQHPRETQMPSSSSQWQRLRLRSKILRSLOAFIAIAR 180  
QY 180 FAHGAATLS 188  
DB 181 FAHGAATLT 189

RESULT 12  
AAB47121  
ID AAB47121 standard; Protein; 196 AA.  
XX  
AC AAB47121;  
XX  
DT 04-JUN-2001 (first entry)  
XX  
XX Murine IL-B30.  
DE  
XX Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;  
KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
KW Castleman's disease.  
XX  
OS Mus musculus.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..196  
FT /note= "Mature protein"  
XX  
XX WO200118051-A2.  
PN  
XX  
XX 15-MAR-2001.  
PD  
XX  
XX 08-SEP-2000; 2000WO-US24686.  
PF  
XX  
XX 09-SEP-1999; 99US-0393090.  
PR 10-NOV-1999; 99US-0164616.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
PI Wiekowski MT, Lira SA, Narula SK;  
XX  
XX WPI: 2001-244560/25.  
DR N-PSDB; AAC85541.  
XX  
XX Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
PT segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
PT atherosclerosis, multiple sclerosis, vasculitis and tumour -  
XX  
PS Disclosure; Page 11-12; 69pp; English.  
XX  
XX This sequence shows mouse interleukin-B30. Fragments of this protein  
CC may be used in the composition of the invention. The composition  
CC comprises a substantially pure polypeptide comprising a number of  
CC distinct segments of at least 7 contiguous amino acids from IL-12 p40  
CC and/or IL-B30, and a substantially pure polypeptide comprising a  
CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
CC IL-B30. The composition is useful for modulating physiology or  
CC development of a cell or tissue in a host organism, resulting in an  
CC increased or decreased production of interferon-gamma (IFNgamma), an  
CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
CC anti-viral effect or antagonized allergic effect, and amelioration  
CC of an autoimmune condition or a chronic inflammatory condition.  
CC IL-B30 or its agonist is useful inducing the proliferation of memory  
CC T-cells. An agonist or antagonist of IL-B30 protein is useful for  
CC modulating the trafficking or activation of a leukocyte in an animal  
CC experiencing science or symptoms of autoimmunity, an inflammatory  
CC condition, tissue specific autoimmunity, degenerative autoimmunity,  
CC rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
CC transplant, spinal injury, stroke, neurodegeneration, an infectious  
CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
CC disease, postmenopausal osteoporosis or IL-6-associated diseases.  
CC IL-12 p40/IL-B30 is useful as an immunogen for the production a  
CC antisera or antibodies specific for binding.



Query Match 46.1%; Score 463; DB 20; Length 102;  
Best Local Similarity 90.0%; Pred. No. 9,le-41;  
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 89 CLQRIHQGLIFVEKLLGSDIFTGPESLPDSPVAQLHASLGLSOLLQPEGHWHWETOQIP 148  
Db 2 CLQRIHQGLIFVEKLLGSDIFTGPESLPDSPVAQLHASLGLSOLLQPEGHWHWETOQIP 61  
QY 149 SLSPSPQWQRLRLKILRSLOAFVAVAAARVFAHGAATLS 188  
Db 62 SPSPSPQWQRLRLKILRSLOAFVAVAAARVFAHGAATLS 101

RESULT 15  
AAB01983  
ID AAB01983 standard; Protein; 102 AA.  
XX AC AAB01983;  
XX DT 27-SEP-2000 (first entry)  
XX DE Mature porcine interleukin-B30 (IL-B30).  
XX KW Interleukin-B30; IL-B30; porcine; pig; cytokine; cellular signalling;  
XX KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
XX KW granulocyte colony stimulating factor; immune disorder;  
XX KW inflammatory disease; autoimmune disease; antigen; antibody.  
XX OS Sus scrofa.  
XX PN US0606284-A.  
XX PD 09-MAY-2000.  
XX PF 24-JUL-1998; 98US-0122443.  
XX PR 25-JUL-1997; 97US-0053765.  
XX PA (SCHE ) SCHERING CORP.  
XX PI Bazan JF;  
XX PS WPI; 2000-364420/31.  
XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30  
XX PT useful as probes or primers for diagnosing immune disorders including  
XX PT autoimmune or chronic inflammatory conditions -

Claim 1; Column 45-46; 32pp; English.  
CC This sequence represents porcine interleukin-B30 (IL-B30). IL-B30  
CC is a novel cytokine, exhibiting significant homology to IL-6 and  
CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical  
CC role in signalling between immune or other cells during an immune  
CC response. The precise role of IL-B30 is not yet known - it is likely to  
CC have either a stimulatory or an inhibitory effect on haematopoietic cells  
CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.  
CC Alternatively, it may affect vascular physiology or development, or have  
CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and  
CC antagonists are useful in the diagnosis and treatment of disorders  
CC associated with abnormal expression or activity of IL-B30 e.g.,  
CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are  
CC useful for recombinant expression of IL-B30 in a host cell, and as a  
CC source of probes and primers. The IL-B30 probes and primers can be used  
CC to detect levels of IL-B30 expression in samples from patients suspected  
CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may  
CC also be used to identify homologous genes in other species. IL-B30  
CC protein or its fragments are useful as antigens for raising antibodies to  
CC various linear and conformational epitopes. Such antibodies may be used  
CC to detect levels of IL-B30 protein in a sample.

XX Sequence\* 102 AA:  
SQ

Query Match 46.1%; Score 463; DB 21; Length 102;  
Best Local Similarity 90.0%; Pred. No. 9,le-41;  
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 89 CLQRIHQGLIFVEKLLGSDIFTGPESLPDSPVAQLHASLGLSOLLQPEGHWHWETOQIP 148  
Db 2 CLQRIHQGLIFVEKLLGSDIFTGPESLPDSPVAQLHASLGLSOLLQPEGHWHWETOQIP 61  
QY 149 SLSPSPQWQRLRLKILRSLOAFVAVAAARVFAHGAATLS 188  
Db 62 SPSPSPQWQRLRLKILRSLOAFVAVAAARVFAHGAATLS 101

Search completed: November 20, 2002, 11:52:59  
Job time : 33.4 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:54:30 ; Search time 7.36364 Seconds  
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Title: US-09-658-699-2  
Perfect score: 1004  
Sequence: 1 MLGSRVALLLLPWTQAQR.....QAFVAVAFVFAHGAATLSP 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	10.1	175	10	US-09-754-532-80
2	101	10.1	175	10	US-09-754-532-87
3	101	10.1	175	10	US-09-754-532-88
4	101	10.1	175	10	US-09-754-532-97
5	100	10.0	175	10	US-09-754-532-79
6	99	9.9	175	10	US-09-754-532-106
7	98	9.8	175	10	US-09-754-532-90
8	97	9.7	175	10	US-09-754-532-89
9	97	9.7	175	10	US-09-754-532-110
10	96	9.6	174	10	US-09-760-008A-1
11	96	9.6	174	10	US-09-950-473-2
12	96	9.6	174	12	US-10-016-403-1
13	96	9.6	174	12	US-10-016-403-2
14	96	9.6	174	12	US-10-003-496-1
15	96	9.6	175	10	US-09-754-532-2
16	96	9.6	175	10	US-09-754-532-68
17	96	9.6	175	10	US-09-754-532-70
18	96	9.6	175	10	US-09-754-532-78
19	96	9.6	175	10	US-09-754-532-83

20	96	9.6	175	10	US-09-754-532-85	Sequence 85, Appl
21	96	9.6	175	10	US-09-754-532-91	Sequence 91, Appl
22	96	9.6	175	10	US-09-754-532-93	Sequence 93, Appl
23	96	9.6	175	10	US-09-754-532-98	Sequence 98, Appl
24	96	9.6	175	10	US-09-754-532-99	Sequence 99, Appl
25	96	9.6	175	10	US-09-754-532-100	Sequence 100, Appl
26	96	9.6	175	10	US-09-754-532-107	Sequence 107, Appl
27	96	9.6	175	10	US-09-754-532-108	Sequence 108, Appl
28	96	9.6	175	10	US-09-230-733-1	Sequence 1, Appl
29	96	9.6	175	10	US-09-818-430A-2	Sequence 2, Appl
30	96	9.6	177	10	US-09-984-186-14	Sequence 14, Appl
31	96	9.6	348	12	US-10-003-496-6	Sequence 6, Appl
32	96	9.6	787	10	US-09-984-186-16	Sequence 16, Appl
33	95	9.5	175	10	US-09-754-532-67	Sequence 67, Appl
34	95	9.5	175	10	US-09-754-532-75	Sequence 75, Appl
35	95	9.5	175	10	US-09-754-532-92	Sequence 92, Appl
36	95	9.5	175	10	US-09-754-532-94	Sequence 94, Appl
37	95	9.5	175	10	US-09-754-532-105	Sequence 105, Appl
38	95	9.5	175	10	US-09-754-532-109	Sequence 109, Appl
39	93.5	9.3	174	12	US-10-016-403-3	Sequence 3, Appl
40	93.5	9.3	175	10	US-09-754-532-86	Sequence 86, Appl
41	93.5	9.3	175	10	US-09-754-532-95	Sequence 95, Appl
42	93.5	9.3	175	10	US-09-754-532-102	Sequence 102, Appl
43	93	9.3	175	10	US-09-754-532-69	Sequence 69, Appl
44	93	9.3	175	10	US-09-754-532-73	Sequence 73, Appl
45	93	9.3	175	10	US-09-754-532-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1  
US-09-754-532-80  
; Sequence 80, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: Amgen Center, 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/754,532  
; FILING DATE:

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/448,716  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol  
; REGISTRATION NUMBER: 34,899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/499-5725  
; TELEFAX: 805/499-8011  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-754-532-80

Query Match 10.1%; Score 101; DB 10; Length 175;

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Best Local Similarity 26.6%; Pred. No. 0.0045;
Matches 49; Conservative 19; Mismatches 76; Indels 40; Gaps 9;

QY 12 LLEWTAQGRAVPGGSPAWTCQQQLSQKSLCTLAWSAHP-----LVGHMDLREEGDETTND 67
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Db 15 LLKCLEQVRKIQDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56

QY 68 VPHICQGCDCDPQGLRDNDSQFCQLRIHQGLFYFEKILGSDIFTG-FPSLLPDSPPVAQLHA 126
   ||      ||      ||      ||      ||      ||      ||      ||      ||      ||
Db 57 IPWAPL-SSCPSSQALQ--LAGLSQLHSGFLPYQGLL--QALEGISPELGTDTDTQLQLDV 111

QY 127 SLGLSQQLLQPGHHWETQQIPSLSPSQ-----PWORLLRFXILKLSQAFAVAAR 178
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Db 112 ADPATTTWQOME-----ELCMAPALQPTOCAMPAPAFASAFQRRAGGVLVASHLQSFLEVSyr 167

QY 179 VFAH 182
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Db 168 VLAH 171
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RESULT 2
US-09-754-532-87
; Sequence 87, Application us/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-87

Query Match 10.1%; Score 101; DB 10; Length 175;
Best Local Similarity 26.6%; Pred. No. 0.0046;
Matches 49; Conservative 19; Mismatches 76; Indels 40; Gaps 9;

QY 12 LLEWTAQGRAVPGGSPAWTCQQQLSQKSLCTLAWSAHP-----LVGHMDLREEGDETTND 67
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Db 15 LLKCLEQVRKIQDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56

QY 68 VPHICQGCDCDPQGLRDNDSQFCQLRIHQGLFYFEKILGSDIFTG-FPSLLPDSPPVAQLHA 126
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Db 57 IPWAPL-SSCPSSQALQ--LAGLSQLHSGFLPYQGLL--QALEGISPELGTDTDTQLQLDV 111

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; Sequence 97, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-97

Query Match 10.1%; Score 101; DB 10; Length 175;
Best Local Similarity 26.6%; Pred. No. 0.0046;
Matches 49; Conservative 19; Mismatches 76; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
Db 15 LLKLAQVRKIQDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
QY 68 VPHIQGDCDQGLRDNSTQFCLORIHQGLIFYEKLKLGSDIFTG-EPSLLPDSFVAQLHA 126
Db 57 IPWAPL-SSCPSQLQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
QY 127 SLGLSQLQPEGHWHWTQIPSLSPSQ-----PWQRLLLRFRKILRSQAFAVAAR 178
Db 112 ADFATTIWQME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYR 167
QY 179 VFAH 182
Db 168 VLRH 171

RESULT 5
US-09-754-532-79
; Sequence 79, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
```

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; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-79

Query Match 10.0%; Score 100; DB 10; Length 175;
Best Local Similarity 26.7%; Pred. No. 0.0058;
Matches 50; Conservative 19; Mismatches 78; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
Db 15 LLKLEQVRKIQDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
QY 68 VPHIQGDCDQGLRDNSTQFCLORIHQGLIFYEKLKLGSDIFTG-EPSLLPDSFVAQLHA 126
Db 57 IPWAPL-SSCPSQLQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
QY 127 SLGLSQLQPEGHWHWTQIPSLSPSQ-----PWQRLLLRFRKILRSQAFAVAAR 178
Db 112 ADFATTIWQME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYR 167
QY 179 VFAH 185
Db 168 VLRH 174

RESULT 6
US-09-754-532-106
; Sequence 106, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09754,532
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match          9.9%; Score 99; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.0074;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQQLSKLCTLANSAHP-----LVGHMDLREGDEETND 67
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Db 15 LKLCLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 VPHIQCGDGDQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTG-EPSSLPPDSPAQLHA 126
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 IPWAPL-SSCPSALQ--LAGCLSOLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 127 SLGLSOLLOPEGHWHETQOIPSLSPSQ-----PWORLLRKFILRSLOAFVAAAR 178
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 AAFATTIWOQME-----ELGAPALOPTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 167
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 VFAH 182
   | |
Db 168 VLRH 171
   | |
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RESULT 7
US-09-754-532-90
; Sequence 90, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-90

Query Match          9.9%; Score 97; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.012;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQQLSKLCTLANSAHP-----LVGHMDLREGDEETND 67
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LKLCLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 VPHIQCGDGDQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTG-EPSSLPPDSPAQLHA 126
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 IPWAPL-SSCPSALQ--LAGCLSOLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 127 SLGLSOLLOPEGHWHETQOIPSLSPSQ-----PWORLLRKFILRSLOAFVAAAR 178
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 AAFATTIWOQME-----ELGAPALOPTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 167
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 VFAH 182
   | |
Db 168 VLRH 171
   | |
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; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-90

Query Match          9.8%; Score 98; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.0093;
Matches 48; Conservative 20; Mismatches 76; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQQLSKLCTLANSAHP-----LVGHMDLREGDEETND 67
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LKLCLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 VPHIQCGDGDQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTG-EPSSLPPDSPAQLHA 126
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 IPWAPL-SSCPSALQ--LAGCLSOLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 127 SLGLSOLLOPEGHWHETQOIPSLSPSQ-----PWORLLRKFILRSLOAFVAAAR 178
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 AAFATTIWOQME-----ELGAPALOPTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 167
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 VFAH 182
   | |
Db 168 VLRH 171
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RESULT 8
US-09-754-532-89
; Sequence 89, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-89

Query Match          9.7%; Score 97; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.012;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQQLSKLCTLANSAHP-----LVGHMDLREGDEETND 67
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LKLCLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 VPHIQCGDGDQGLRDNSQFCQLRIHQGLIFYEKLLGSDIFTG-EPSSLPPDSPAQLHA 126
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 IPWAPL-SSCPSALQ--LAGCLSOLHSGFLYQGLL--QALEGISPELGTDLTLDLQDV 111
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 127 SLGLSOLLOPEGHWHETQOIPSLSPSQ-----PWORLLRKFILRSLOAFVAAAR 178
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 AAFATTIWOQME-----ELGAPALOPTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 167
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 179 VFAH 182
   | |
Db 168 VLRH 171
   | |
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Db 15 LKCLEQVRKIOGAGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 56  
QY 68 VPHIOCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 57 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTQLD 111  
QY 127 SLGLSOLLQPEGHWHWTQQIPSLSPSQ-----PWQRLLLRFRKILRSLOAFVAA 178  
Db 112 ADFATTIWOQME-----ELGMAPALQPTOGAMPAPAFASAFQRRAGGVLVASHLQSFLEVS 167  
QY 179 VFAH 182  
Db 168 VLRH 171

RESULT 9  
US-09-754-532-110  
; Sequence 110, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: Amgen Center, 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09754,532  
; APPLICATION NUMBER: US/09754,532  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/448,716  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fesslin, Karol  
; REGISTRATION NUMBER: 34,899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/499-5725  
; TELEFAX: 805/499-8011  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-754-532-110

Query Match 9.7%; Score 97; DB 10; Length 175;  
Best Local Similarity 26.1%; Pred. No. 0.012;  
Matches 48; Conservative 20; Mismatches 76; Indels 40; Gaps 9;  
QY 12 LLPWTAQGRAVPGGSSPAWTCQQLSQKLCITLANSAP-----LVGHMDLREEGDEETND 67  
Db 15 LKCLEQVRKIOGAGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 56  
QY 68 VPHIOCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 57 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTQLD 111  
QY 127 SLGLSOLLQPEGHWHWTQQIPSLSPSQ-----PWQRLLLRFRKILRSLOAFVAA 178  
Db 112 ADVATTIWOQME-----ELGMAPALQPTOGAMPAPAFASAFQRRAGGVLVASHLQSFLEVS 167

QY 179 VFAH 182  
Db 168 VLRH 171

RESULT 10  
US-09-760-008A-1  
; Sequence 1, Application US/09760008A  
; Patent No. US20020004483A1  
; GENERAL INFORMATION:  
; APPLICANT: NISSEN, TORBEN LAUESGAARD  
; APPLICANT: ANDERSEN, KIM VILBOUR  
; APPLICANT: HANSEN, CHRISTIAN KARSTEN  
; APPLICANT: MIKKELSEN, JAN MOLLER  
; TITLE OF INVENTION: G-CSF CONJUGATES  
; FILE REFERENCE: 31-000700US  
; CURRENT APPLICATION NUMBER: US/09760,008A  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/176,376  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/189,506  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/215,644  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DK PA 2000 00024  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: DK PA 2000 00341  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: DK PA 2000 00943  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-008A-1

Query Match 9.6%; Score 96; DB 10; Length 174;  
Best Local Similarity 26.1%; Pred. No. 0.015;  
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;  
QY 12 LLPWTAQGRAVPGGSSPAWTCQQLSQKLCITLANSAP-----LVGHMDLREEGDEETND 67  
Db 14 LKCLEQVRKIOGDGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 55  
QY 68 VPHIOCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 56 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTQLD 110  
QY 127 SLGLSOLLQPEGHWHWTQQIPSLSPSQ-----PWQRLLLRFRKILRSLOAFVAA 178  
Db 111 ADFATTIWOQME-----ELGMAPALQPTOGAMPAPAFASAFQRRAGGVLVASHLQSFLEVS 166  
QY 179 VFAH 182  
Db 167 VLRH 170

RESULT 11  
US-09-950-473-2  
; Sequence 2, Application US/09950473  
; Patent No. US20020151488A1  
; GENERAL INFORMATION:  
; APPLICANT: Sarkar, Casim  
; APPLICANT: Laufienburger, Douglas  
; TITLE OF INVENTION: G-CSF Analog Compositions and Methods  
; FILE REFERENCE: 01017/37732  
; CURRENT APPLICATION NUMBER: US/09/950,473  
; CURRENT FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2

US-10-016-403,1

US-10-016-403-2

QY 12 LLPWTAQGRAVPGSSPAWTCOCOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67  
DB 14 LKLCLEQVRKIOGDGA-----ALQEKLCATYKLCHPBELVLLGH-----SLG 55  
QY 68 VPHIQCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126  
DB 56 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGPDLTLQLDV 110  
QY 127 SLGLSQLLOPEGHWHWTQIPSLPSQ-----PWQRLLRFKILRSLOAFVAVAR 178  
DB 111 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYR 166  
QY 179 VFAH 182  
DB 167 VLRH 170

RESULT 14  
US-10-003-496-1  
; Sequence 1, Application US/10003496  
; Patent No. US20020142964A1  
; GENERAL INFORMATION:  
; APPLICANT: Maxygen Aps  
; TITLE OF INVENTION: Single-Chain Polypeptides  
; FILE REFERENCE: 0218US210  
; CURRENT APPLICATION NUMBER: US/10/003,496  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 60/245,727  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-003-496-1

Query Match 9.6%; Score 96; DB 12; Length 174;  
Best Local Similarity 26.1%; Pred. No. 0.015;  
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;  
QY 12 LLPWTAQGRAVPGSSPAWTCOCOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67  
DB 14 LKLCLEQVRKIOGDGA-----ALQEKLCATYKLCHPBELVLLGH-----SLG 55  
QY 68 VPHIQCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126  
DB 56 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGPDLTLQLDV 110  
QY 127 SLGLSQLLOPEGHWHWTQIPSLPSQ-----PWQRLLRFKILRSLOAFVAVAR 178  
DB 111 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYR 166  
QY 179 VFAH 182  
DB 167 VLRH 170

RESULT 15  
US-09-754-532-2  
; Sequence 2, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Angen Inc.  
; STREET: Angen Center, 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California

COUNTRY: United States of America  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/754,532  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/448,716  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pessin, Karol  
REGISTRATION NUMBER: 34,899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 805/499-5725  
TELEFAX: 805/499-8011  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-754-532-2

Query Match 9.6%; Score 96; DB 10; Length 175;  
Best Local Similarity 26.1%; Pred. No. 0.015;  
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;  
QY 12 LLPWTAQGRAVPGSSPAWTCOCOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67  
DB 15 LKLCLEQVRKIOGDGA-----ALQEKLCATYKLCHPBELVLLGH-----SLG 56  
QY 68 VPHIQCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126  
DB 57 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGPDLTLQLDV 111  
QY 127 SLGLSQLLOPEGHWHWTQIPSLPSQ-----PWQRLLRFKILRSLOAFVAVAR 178  
DB 112 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYR 167  
QY 179 VFAH 182  
DB 168 VLRH 171

Search completed: November 20, 2002, 12:00:55  
Job time : 8.36364 secs



Result No.	Query			ID	Description	
	Score	Match	Length			
1	1004	100.0	189	3	US-09-122-443-2	Sequence 2, Appli
2	718.5	71.6	196	3	US-09-122-443-4	Sequence 4, Appli
3	463	46.1	102	3	US-09-122-443-5	Sequence 5, Appli
4	102	10.2	307	3	US-08-469-318-121	Sequence 121, App
5	102	10.2	307	3	US-08-469-318-122	Sequence 122, App
6	102	10.2	307	3	US-08-469-318-134	Sequence 134, App
7	102	10.2	307	3	US-08-469-318-135	Sequence 135, App
8	102	10.2	307	3	US-08-468-609A-121	Sequence 121, App
9	102	10.2	307	3	US-08-468-609A-122	Sequence 122, App
10	102	10.2	307	3	US-08-468-609A-134	Sequence 134, App
11	102	10.2	307	3	US-08-468-609A-135	Sequence 135, App
12	102	10.2	307	4	US-08-446-872A-121	Sequence 121, App
13	102	10.2	307	4	US-08-446-872A-122	Sequence 122, App
14	102	10.2	307	4	US-08-446-872A-134	Sequence 134, App
15	102	10.2	307	4	US-08-446-872A-135	Sequence 135, App
16	102	10.2	307	4	US-08-762-227A-121	Sequence 121, App
17	102	10.2	307	4	US-08-762-227A-122	Sequence 122, App
18	102	10.2	307	4	US-08-762-227A-134	Sequence 134, App
19	102	10.2	307	4	US-08-762-227A-135	Sequence 135, App
20	102	10.2	307	5	PCF-US95-01185-121	Sequence 121, App
21	102	10.2	307	5	PCF-US95-01185-122	Sequence 122, App
22	102	10.2	307	5	PCF-US95-01185-134	Sequence 134, App
23	102	10.2	307	5	PCF-US95-01185-135	Sequence 135, App
24	101	10.1	175	1	US-08-010-099-80	Sequence 80, Appli
25	101	10.1	175	1	US-08-010-099-87	Sequence 87, Appli
26	101	10.1	175	1	US-08-010-099-88	Sequence 88, Appli
27	101	10.1	175	1	US-08-010-099-97	Sequence 97, Appli

QY	1	MLGSRAVMILLLLPWTQAQRAVPGSSPWATCOOQSQKCTLAWSAHPVLVGHMD-LRRE	59
Db	1	MLDCRAVIMLWLLPWTQGLAVPRSSPDWAQCOOLSRNLCMLAWNAHAPAGHMNLRRE	60
QY	60	GDEETINDVPHIQCGDGPQGLRDNSQFCQRTHQGLIFYEKKLLGSDITGTPSLLPDS	119
Db	61	EDEETKNVPRIQDCCDPQGLKNSQFCQRIRQGLAFYKHLDSDFEKGEPALLPS	120
QY	120	PVAQLHASLLGLSQLPQEGHHWETQOTPSLSPSPQWQRLLRKILRSQAQFAVAARY	179
Db	121	PMEQLHTSLGLSQLPQEDHPRETQOMPSLSSSQWQRPRLRSKILRSQAQLAIAARY	180
QY	180	FAHGAATLS 188	

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RESULT 4
US-08-469-318-121
; Sequence 121, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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;
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-318-135

Query Match 10.2%; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

QY 15 WTAQGRAVPGSS-----PAWTQCOQ-----LSQKLCITLAW 45
; :||| ||| : : : : : : : : : : : : : : : : : :
Db 114 YVIEGRISPGGGGGGNNATPLGPASSLPQSFLKLSQVQRKIQGDGAALQEKLCATYK 173
; :||| ||| : : : : : : : : : : : : : : : : : :
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDGPQGLRDNQSFCLQRIHOGGLIFYE 101
; :||| : : : : : : : : : : : : : : : : : :
Db 174 LCHPEELVLGH-----SLGIPWAPL--SSCPSQALQ--LAGCLSQLHSGSLFLYQ 219
; :||| : : : : : : : : : : : : : : : : : :
QY 102 KILGSDIFTG-EPSLLPSPVAQLHASLLGLSQLLOPEGHWHWETQOIPSLSPSQ----- 154
; :||| : : : : : : : : : : : : : : : : : :
Db 220 GLL--QALEGISPELGTDLTDLQDVADFATTIQQME-----ELGMAPALQPTOGAMPAP 273
; :||| : : : : : : : : : : : : : : : : : :
QY 155 --PWQRLLRFKILRSLOAFVAARVFAH 182
; :||| : : : : : : : : : : : : : : : : : :
Db 274 ASAFQRRAGGVLVASHLQSFLEVSRYRLRH 303
; :||| : : : : : : : : : : : : : : : : : :

RESULT 8
US-08-468-609A-121
; Sequence 121, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-609A-121

Query Match 10.2%; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

QY 15 WTAQGRAVPGSS-----PAWT-----QCQO-----LSQKLCITLAW 45
; :||| ||| : : : : : : : : : : : : : : : : : :
Db 114 YVIEGRISPGGGGGGNNATPLGPASSLPQSFLKLSQVQRKIQGDGAALQEKLCATYK 173
; :||| ||| : : : : : : : : : : : : : : : : : :
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDGPQGLRDNQSFCLQRIHOGGLIFYE 101
; :||| : : : : : : : : : : : : : : : : : :
Db 174 LCHPEELVLGH-----SLGIPWAPL--SSCPSQALQ--LAGCLSQLHSGSLFLYQ 219
; :||| : : : : : : : : : : : : : : : : : :
QY 102 KILGSDIFTG-EPSLLPSPVAQLHASLLGLSQLLOPEGHWHWETQOIPSLSPSQ----- 154
; :||| : : : : : : : : : : : : : : : : : :
Db 220 GLL--QALEGISPELGTDLTDLQDVADFATTIQQME-----ELGMAPALQPTOGAMPAP 273
; :||| : : : : : : : : : : : : : : : : : :
QY 155 --PWQRLLRFKILRSLOAFVAARVFAH 182
; :||| : : : : : : : : : : : : : : : : : :
Db 274 ASAFQRRAGGVLVASHLQSFLEVSRYRLRH 303
; :||| : : : : : : : : : : : : : : : : : :

RESULT 9
US-08-468-609A-122
; Sequence 122, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/468,609A  
APPLICATION NUMBER: US/08/468,609A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-609A-122

Query Match 10.2%; Score 102; DB 3; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;  
QY 15 WTAOGRVPGGSS-----PAWTQCCQ-----LSOKLCTLAW 45  
DB 114 VYIEGRISPGGGSGGSMATPLGPASSLPQSFLKSLQVRKIQDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEDDETTNDVPHIQCGDGPQGLRDNRSQFCLORIHQGLIFYE 101  
DB 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSQLHSGFLYQ 219  
QY 102 KLGSDFITG--EPSLLPDPSPVAQLHASLLGSLQLQPEGHWHWETQIIPSLSPSQ----- 154  
DB 220 GLL--QALEGISPELGPFTLDTLQDLDVADFATTIWOQME-----ELGMAPALQPTQGAMP 273  
QY 155 ---PWORLLRKFILRSLOAFVAVAAARFAH 182  
DB 274 ASAFORRAGGVLVASHLQSFLEVSRYVLRH 303

RESULT 10  
US-08-468-609A-134  
Sequence 134, Application US/08468609A  
Patent No. 6030812  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Mair H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESS: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM: Floppy disk  
MEDIUM TYPE:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/468,609A  
APPLICATION NUMBER: US/08/468,609A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-609A-134

Query Match 10.2%; Score 102; DB 3; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;  
QY 15 WTAOGRVPGGSS-----PAWT-----CQCC-----LSOKLCTLAW 45  
DB 114 VYIEGRISPGGGSGGSMATPLGPASSLPQSFLKSLQVRKIQDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEDDETTNDVPHIQCGDGPQGLRDNRSQFCLORIHQGLIFYE 101  
DB 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSQLHSGFLYQ 219  
QY 102 KLGSDFITG--EPSLLPDPSPVAQLHASLLGSLQLQPEGHWHWETQIIPSLSPSQ----- 154  
DB 220 GLL--QALEGISPELGPFTLDTLQDLDVADFATTIWOQME-----ELGMAPALQPTQGAMP 273  
QY 155 ---PWORLLRKFILRSLOAFVAVAAARFAH 182  
DB 274 ASAFORRAGGVLVASHLQSFLEVSRYVLRH 303

RESULT 11  
US-08-468-609A-135  
Sequence 135, Application US/08468609A  
Patent No. 6030812  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Mair H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESS: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-609A-135

Query Match      10.2%; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

QY 15 WTAQGRAVPGSS-----PAWTCQQ-----LSOKLCTLAW 45
DB 114 YVIEGRTPSGGGGGNNATPLGPASSLPQLSLKSLQVNRKIQDGAALQEKLCATYK 173
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHTQCQGDGDPQLGRDNSQFCIQRIHQGLIFYE 101
DB 174 LCHPELVLLGH-----SLGIPWAPL--SSCPSSQALQ--LAGCLSQLHSGLFLYQ 219
QY 102 KILGSDITFG--EPSLLPDSVPAQLHASLLGSLQLLQPEGHHWETQIPSLSPSQ----- 154
DB 220 GLL--QALEGISPELGPETLDTQLDQVADFATTWQQE-----ELGMAPALQPTQGMFAF 273
QY 155 --PMWRLLLRFKILRSIQAFVAVAARVFAH 182
DB 274 ASAFORRAGGVLVASHLQSFLEVSRYVLRH 303

RESULT 12
US-08-446-872A-121
; Sequence 121, Application US/08446872A
; Patent No. 6361577
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Orlins, Peter O.
; APPLICANT: Paik, Kumnan
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivalent IL-3 Hematopoiesis
; TITLE OF INVENTION: Fusion Protein
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

```

STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-872A-122

Query Match 10.2%; Score 102; DB 4; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;  
QY 15 WTAQGRAVPGSS-----PWTQCOQ-----LSOKLCTLAW 45  
Db 114 YVIEGRISPGGGGGNNATPLGPASSLPQSLKLSLEQVRKIQGDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDGPQGLRDNQFCQRIHQGLIFYE 101  
Db 174 LCHPEELVLLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSLSGLFLYQ 219  
QY 102 KLLGSDIFTG-EPSLLPDPSPAQLHASLLGLSOLLQPEGHWHWTQIPLSPSQ-----154  
Db 220 GLL--QALEGISPELGLPTLDTLQLDVADFATTIWOOME-----ELGMAPALQPTQAMPAPF 273  
QY 155 --PWQRLRLRFKILRSLOAFVAVAAARVFAH 182  
Db 274 ASAFQRRAGGVIVASHLOSFLVSVYRLRH 303

RESULT 14  
US-08-446-872A-134  
Sequence 134, Application US/08446872A  
Patent No. 6361977  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Maire H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.

STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-872A-134  
Query Match 10.2%; Score 102; DB 4; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;  
QY 15 WTAQGRAVPGSS-----PWT-----QCOQ-----LSOKLCTLAW 45  
Db 114 YVIEGRISPGGGGGNNATPLGPASSLPQSLKLSLEQVRKIQGDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDGPQGLRDNQFCQRIHQGLIFYE 101  
Db 174 LCHPEELVLLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSLSGLFLYQ 219  
QY 102 KLLGSDIFTG-EPSLLPDPSPAQLHASLLGLSOLLQPEGHWHWTQIPLSPSQ-----154  
Db 220 GLL--QALEGISPELGLPTLDTLQLDVADFATTIWOOME-----ELGMAPALQPTQAMPAPF 273  
QY 155 --PWQRLRLRFKILRSLOAFVAVAAARVFAH 182  
Db 274 ASAFQRRAGGVIVASHLOSFLVSVYRLRH 303  
RESULT 15  
US-08-446-872A-135  
Sequence 135, Application US/08446872A  
Patent No. 6361977  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Maire H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-872A-135

Query Match 10.2%; Score 102; DB 4; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;  
QY 15 WTAQGRAVPGSS-----PAWTCQQ-----LSQKLCGLAW 45  
Db 114 YVIEGRISPGSGGSGSNMATPLGPASSLPQSFLKLSLEQVRKIQDGAALQERKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHTCQCGDQDQGLRDNSQFCLQRIHQGLIFYE 101  
Db 174 LCHPEELVLGH-----SLGIPWAPL-SSCPSQALQ--LACCLSLHSGFLFYQ 219  
QY 102 KLLGSDIFTG-EPSLLPDSVPAQLHASLLGLSOLLQLEPEGHWHETQOIPSLSPSQ----- 154  
Db 220 GLL--QALEGISPELGPDTLDTQLDVAADFATTIQQME----ELGMAPALQPTQGAMPAF 273  
QY 155 --PWQRLLLRFKILRSLOAFVAVAF 182  
Db 274 ASAFQRRAGGVLVASHLQSELEVSIVRLRH 303

Search completed: November 20, 2002, 12:00:12  
Job time : 13.7818 secs



Query Match		10.6%;	Score 110;	DB 1;	Length 208;
Best Local Similarity		25.5%;	Pred. No. 0.0051;		
Matches		51;	Conservative	27;	Mismatches 84; Indels 38; Gaps 8;
QY	8	IMLWLLPWVTOGLIAPVRSSSPDWAQ	COQLSRNLCLMLAWNAHAPAGH	-----MNLRL	-----E 59
Db	14	VSLGLLLVMTSAFFPGPLGEDFKNDTTP	SRLLTTPTEKTEALIKHIVDKISAIRKEICE	73	
QY	60	EEDP	-----ETKNNVPRIQCEGCDPQGLKNSQFC	QRIQROGLAFYKHLDD	--SD 108
Db	74	KNDECNSKETTAENKLIKLPKMEKDKGCFQSGF	--NQAVCLIKTTAGLLEYQIYLDLFQ	LN 131	
QY	109	IFKGEFALLPDSMPMEOLHTSLGLSOLLQ	-----PEDHPRETQOMPSLSSSQOWOR	159	
Db	132	EFEFN	-----QETVMELOQSIRTLQILKEKTAGLITTPATH	---TDLLEKMQSSNEWVK	183
QY	160	PLLRSKILRSLOAFLAIAAR	179		
Db	184	NAKVIIILRSLENFLQFLRLR	203		
RESULT 3					
A56610					
interleukin-6 precursor - bovine					
C:Species: Bos primigenius taurus (cattle)					
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999					
R:Roogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.					
DNA Seq. 2, 411-413, 1992					
A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.					
A:Reference number: A56610; MUID:93076003; PMID:1446077					
A:Accession: A56610					
A>Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-208 <DRO>					
A:Cross-references: EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194					
A:Experimental source: BLV induced B cell-lymphosarcoma					
A:Note: sequence extracted from NCBI backbone (NCBIP:118917)					
A:Superfamily: interleukin-6					
C:Keywords: cytokine					
Query Match		10.0%;	Score 104;	DB 1;	Length 208;
Best Local Similarity		26.8%;	Pred. No. 0.019;		
Matches		37;	Conservative	23;	Mismatches 54; Indels 24; Gaps 5;
QY	59	EEDP	-----ETKNNVPRIQCEGCDPQGLKNSQFC	QRIQROGLAFYKHLDD	--S 107
Db	73	EKNDECSSKETTAENKLNLPKMEKDKGCFQSGF	--NQAICLRTTAGLLEYQIYLDYIQ	130	
QY	108	DIFKGEFALLPDSMPMEOLHTSLGLSOLLQ	P	-----DHPRETQOMPSLSSSQOWORPL	161
Db	131	NEYEGNQENVRD	-----LRKNIRTLQILKQKIADLTITPATNTD	LLEKMQSSNEWVKNA	185
QY	162	LRSKILRSLOAFLAIAAR	179		
Db	186	KIILILRNLENFLQFSLR	203		
RESULT 4					
S02766					
Pulmonary surfactant protein B precursor - rat					
C:Species: Rattus norvegicus (Norway rat)					
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999					
R:Emrie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.					
Biochim. Biophys. Acta 994, 215-221, 1989					
A:Title: cDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfactant protein B					
A:Reference number: S02766; MUID:89150284; PMID:2920185					
A:Accession: S02766					
A:Molecule type: mRNA					
A:Residues: 1-376 <EMR>					
A:Cross-references: EMBL:X14778; NID:g57284; PIDN:CAA32885.1; PID:g57285					
C:Superfamily: Pulmonary surfactant protein B; saposin repeat homology					
F;1-19/Domain: signal sequence #status predicted <SIG>					
F;20-190/Domain: propeptide #status predicted <PRO>					
F;59-151/Domain: saposin repeat homology <SAP1>					
F;190-277/Domain: saposin repeat homology <SAP2>					
F;191-269/Domain: pulmonary surfactant protein B #status predicted <MAT>					
F;286-371/Domain: saposin repeat homology <SAP3>					
Query Match		9.8%;	Score 101.5;	DB 2;	Length 376;
Best Local Similarity		29.3%;	Pred. No. 0.068;		
Matches		55;	Conservative	22;	Mismatches 70; Indels 41; Gaps 11;
QY	10	LWLPLPWV-TQGLAPVRSSSPDWAQ	-----COQLSRNL	-----CMLAWNAHAPAGHM	-- 54
Db	9	LLLLPTCLSLGATASASPDCAGPKFWCQSL	EQALQCRALGHCLQEVWGHAGANDLCQ	68	
QY	55	-----NLLREEDEETKNNVPRIQCEGCDPQGLKNSQFC	QRIQROGLAFYKHLDD	108	
Db	69	ECEDIVHLTLTKMTKEDAFQDTIRKFL	EQECDILPLK	-----LLVPRCQVLDVYLPV-ID	123
QY	109	IFKGEFALLPDSMPMEOLHTSLGLSOLLQ	P	-----DHPRETQOMPSLSSSQOWORPLLRSKILR	168
Db	124	YFQGG--IKPKAICS--HVGLCPLGQ	-TKPEQKPEMLDAIPN	-----PLINKLVLP	169
QY	169	SLQ-AFLA	175		
Db	170	ALPGAFLA	177		
RESULT 5					
I46621					
Pinterleukin 6 - pig					
C:Species: Sus scrofa domestica (domestic pig)					
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999					
R:Richards, C.; Saklatva, J.					
Cytokine 3, 269-276, 1991					
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression					
A:Reference number: I46621; MUID:9138547; PMID:1873476					
A:Accession: I46621					
A>Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: mRNA					
A:Residues: 1-212 <RIC>					
A:Cross-references: GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625					
C:Genetics:					
A:Gene: IL6					
C:Superfamily: interleukin-6					
Query Match		9.6%;	Score 100;	DB 2;	Length 212;
Best Local Similarity		25.0%;	Pred. No. 0.047;		
Matches		39;	Conservative	22;	Mismatches 57; Indels 38; Gaps
QY	52	GHMNLREEDE	-----ETKNNVPRIQCEGCDPQGLKNSQFC	QRIQROGL	98
Db	62	GKISAMRKEMCEKYEKCNSEKVEILAENNLNLPKMAEKDGC	QSGF--NOETCLMRITITGL	119	
QY	99	AFYKHLDD	-----SDIFKGEFALLPDSMPMEOLHTSLGLSOLLQ	P	-----DHPRETQOMPS
Db	120	VEFYIYLDYLOKEYESNKN	-----VEAVQISTKALIQTLROKGNPKATTPNPTT	171	
QY	151	-----LSSSQOWORPLLRSKILRSLOAFLAIAAR	179		
Db	172	NAGLLDKLQSQNEWMKNTKIILRSLEDFLQFSLR	207		
RESULT 6					
interleukin 6 - pig					
C:Species: Sus scrofa domestica (domestic pig)					
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999					
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.					
Mol. Reprod. Dev. 32, 324-330, 1992					
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co					

A;Residues: 1-211 <GRE>  
A;Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728  
R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.  
Biochem. Biophys. Res. Commun. 166, 139-145, 1990  
A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleav  
A;Reference number: A90157; MUID:90147691; PMID:2302197  
A;Accession: E34047  
A:Molecule type: protein  
A;Residues: 66-69,'X','71-75;78-94;128-148 <JA5>  
R;Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; S  
proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986  
A;Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lympho  
A;Reference number: A26662; MUID:87092311; PMID:2948184  
A;Accession: A26662  
A:Molecule type: protein  
A;Residues: 25-39,'X','41-42,'X','44-45 <VSN>  
R;Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.  
proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988  
A;Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA  
A;Reference number: A40486; MUID:89017145; PMID:3262872  
A;Accession: A40486  
A:Molecule type: mRNA  
A;Residues: 1-211 <CHI>  
A;Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410  
R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.  
Blood 72, 2070-2073, 1988  
A;Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleuki  
A;Reference number: A60799; MUID:89062753; PMID:3264198  
A;Accession: A60799  
A:Molecule type: protein  
A;Residues: 77-98 <SHA>  
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.  
J. Exp. Med. 171, 965-970, 1990  
A;Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a  
A;Reference number: SI0241; MUID:90171860; PMID:2106569  
A;Accession: SI0241  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-6 <BLA>  
A;Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860  
R;Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.  
Eur. J. Biochem. 217, 53-59, 1993  
A;Title: Specific covalent modification of the tryptophan residues in murine interleu  
A;Reference number: S38254; MUID:94039075; PMID:8223586  
A;Accession: S38254  
A;Status: preliminary  
A:Molecule type: protein  
A;Residues: 38-60;75,'X',77-79;176-203 <ZHA>  
C;Genetics:  
A;Gene: IL-6  
A;Map position: 5  
A;Introns: 7/1; 68/3; 106/3; 156/3  
C;Superfamily: Interleukin-6  
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokin  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-211/Product: interleukin-6 #status experimental <MA>

	Query Match	Best Local Similarity	Matches	Conservative	Score	DB 1:	Length	DB 2:	Gaps
QY	35	QLSRNLCLAWNAHAPAGHMNLLREEDDEETKNN--VPRIQCEGDCDPOGLKNSQFCIQ	92	:	: :	:	:	:	:
Db	64	EMRKELC-----NGNSDC--MN-----NDDAENLNKLPEIQRNDGCYCQTGY--NQEICLL	111	:	:	:	:	:	:
QY	93	RIRGOAFYKHLLD-----SDIFKGEPALIP-----DSPMEQLMTSL--GLSQ	134	:	:	:	:	:	:
Db	112	KISSGLLEYSHYLEYMKNLNKDKNKARVLQRTDTLIHFNQEVKDLHKIVLPPTISN	171	:	:	:	:	:	:
QY	135	LLOPEDHPRETQQMPSUSSSQOQWRPLLRSKILRSLOAFIAAAR	179	:	:	:	:	:	:
Db	172	ALLTD-----KLESQEWLRTKTIOFLKSLEEFKVTLR	206	:	:	:	:	:	:

```
RESULT 8
A34247
interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derive
A:Reference number: A34247; MUID:89380206; PMID:2789217
A:Accession: A34247
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NOR>
A:Cross-references: GB:M36744; NID:g204915; PIDN:AAA77659.1; PID:g204916
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match      8.8%; Score 91; DB 2; Length 211;
Best Local Similarity 24.5%; Pred. No. 0.33;
Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;

QY 35 QLSRNLCMLAWNAHAPAGHNNLLREEDEETKNN--VPRIQCEGCDPQGLKDNSQFCLO 92
DB 64 EMRKELC---NGNSDC---MN---SDDALSENNUKLPRIQNDGCFQGY--NQEICLL 111
QY 93 RIRQGLAFYKHLID-----SDIFKGEALLPDPSPMEQLHTSLGLSLLQQLQEDH---PR 143
DB 112 KICSGLLFRFFLYEFYKNNLDKNKDKARVIOSTETLVIH---FKQEIKDSYKIVLPT 167
QY 144 ETQQ-----MPSLSQQQWQRPILRSKILRSIQAFIAAR 179
DB 168 PTSNALLMEKLESQEWLRTKTIQLILKALEBFLKVTMR 206

RESULT 9
T09255
granulocyte colony-stimulating factor precursor - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
C:Accession: T09255
R:Dunham, S.P.; Onions, D.E.
submitted to the EMBL Data Library, September 1996
A:Description: Cloning, sequence and expression of feline granulocyte colony stimulating
A:Reference number: Z16630
A:Accession: T09255
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-194 <DUN>
A:Cross-references: EMBL:X08558
C:Function:
A:Description: stimulates the differentiation and proliferation of hematopoietic progenit
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; macrophage
F:1-20/domain: signal sequence (fragment) #status predicted <SIG>
F:21-194/product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match      8.3%; Score 86.5; DB 2; Length 194;
Best Local Similarity 28.3%; Pred. No. 0.8;
Matches 34; Conservative 20; Mismatches 51; Indels 15; Gaps 5;

QY 78 CDPOGLKDNSQFCLOIRQGLAFYKHLSDIFKGEALLPDPSPMEQLHTSLGLSLLQQLQ 137
DB 84 CSSQALQLTG--CLIRQHSGLFYQGLLQQA--LAGISPELAPTLDMLQLDITDFAINWQQ 140
QY 138 PED-----HPRETQQMPSSLSSQQWQRPILRSKILRSIQAFIAARFAHGAATLTTP 191
DB 141 MEDVGMAPVPPTQGTMTFTSA--FQRRAGGTIVASNLQSFLEVAYRALRH----FTRP 194

RESULT 10
C96711
F24J5.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96711
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96711
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <STO>
A:Cross-references: GB:AE005173; NID:g5734711; PIDN:AAD49976.1; GSPDB:GN001
C:Genetics:
A:Gene: F24J5.9
A:Map position: 1

Query Match      8.3%; Score 86.5; DB 2; Length 353;
Best Local Similarity 26.2%; Pred. No. 1.7;
Matches 43; Conservative 20; Mismatches 48; Indels 53; Gaps 9;

QY 26 SSP-----DNAQCOQLSRNLCMLAWNAHAPAGHNNLLREEDEETKNNVPRIQCEG 77
DB 104 SSPELVNNKSDMLRSVOL-----WN-HSP-----DLNPKKEERVAKKAVVEKPSG 150
QY 78 C-DPQGLKDNSQFCLOIRQGLAFYKHLSDIFKGEALLPDPSPMEQLHTSL-----G 131
DB 151 AFQP-----FQKRVLDTL---QPAVKVASSMPATTTSTTETCGG 188
QY 132 LSQQLQPDHPRETQQMPSSLSSQQWQRPILRSKILRSIQ 171
DB 189 KSDLIKAGDEERRTEQQSQSHTHKQRCWSPHRRFLNALQ 232

RESULT 11
A36028
DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces ce
N:Alternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A36028; B36028; S60919; S63235; S65121
R:Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Cell 62, 1143-1151, 1990
A:Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A:Reference number: A36028; MUID:90381771; PMID:2169349
A:Accession: A36028
A:Molecule type: DNA
A:Residues: 1-2222 <MOR>
A:Cross-references: GB:M60416; GB:M36724; NID:gl71408; PIDN:AAA88711.1; PID:gl71409
A:Accession: B36028
A:Molecule type: protein
A:Residues: 1214-1216, 'X', 1218-1221 <MOR>
R:Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV
A:Reference number: S60909
A:Accession: S60919
A:Molecule type: DNA
A:Residues: 1-2221 <SEN>
A:Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
R:Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63235
A:Accession: S63235
A:Molecule type: DNA
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RESULT 13  
IVHUB2  
Interleukin-6 precursor [validated] - human  
N:Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell on factor  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 08-Dec-2000  
C:Accession: A32648; A26962; A26966; A33515; A25801; A25921; I52193; I56003; A27601;  
R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi  
EMBO J. 6, 2939-2945, 1987  
A:Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g  
A:Reference number: A32648; MUID:88082664; PMID:3500852  
A:Accession: A32648  
A:Molecule type: DNA  
A:Residues: 1-212 <YAS>  
A:Cross-references: GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495  
A:Note: the authors translated the codon CAG for residue 130 as Glu  
R:Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.  
EMBO J. 5, 2529-2537, 1986  
A:Title: Structure and expression of cDNA and genes for human interferon-beta-2 and a di  
A:Reference number: A91051; MUID:87053818; PMID:3023045  
A:Accession: A25692  
A:Molecule type: mRNA  
A:Residues: 1-212 <ZIL>  
A:Cross-references: GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674  
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwam  
i, T.; Kishimoto, T.  
Nature 324, 73-76, 1986  
A:Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph  
A:Reference number: A93387; MUID:87065033; PMID:3491322  
A:Accession: A26966  
A:Molecule type: mRNA  
A:Residues: 1-212 <HIR>  
A:Cross-references: GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850  
R:Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.  
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989  
A:Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization  
A:Reference number: A33515; MUID:89391938; PMID:2789513  
A:Accession: A33515  
A:Molecule type: mRNA  
A:Residues: 1-212 <TON>  
A:Cross-references: GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063  
R:Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.  
Eur. J. Biochem. 159, 625-632, 1986  
A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein i  
A:Reference number: A25801; MUID:87004683; PMID:3758081  
A:Accession: A25801  
A:Molecule type: DNA; mRNA  
A:Residues: 1-212 <HAE>  
A:Cross-references: GB:X04403  
A:Experimental source: fibroblast  
R:May, L.T.; Hellgott, D.C.; Sehgal, P.B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986  
A:Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 m  
A:Reference number: A25921; MUID:87067433; PMID:3538015  
A:Accession: A25921  
A:Molecule type: mRNA  
A:Residues: 1-212 <MAY>  
A:Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910

A;Wong, G.C.; Mitek, G.; Glick, D.; Newkirk, R.R.; Clark, J.C.; Ogawa, N.; Behring Inst. Mil. 83, 40-47, 1988

A;Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.

A;Reference number: I52193; MUID:89193317; PMID:3266463

A;Accession: I52193

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-212 <WON>

A;Cross-references: GB:M54894; NID:g186351; PIDN:AAC1704.1; PID:g186352

E;Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.

J. Immunol. 139, 4116-4121, 1987

A;Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*.

A;Reference number: I56003; MUID:88088768; PMID:3320204

A;Accession: I56003



Search completed: November 20, 2002, 11:55:02  
Job time : 16.7636 secs





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FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 11.1%; Score 115; DB 1; Length 208;
Best Local Similarity 25.5%; Pred. No. 0.00059;
Matches 51; Conservative 28; Mismatches 83; Indels 38; Gaps 8;

QY 8 IMWLPLPWTOGLAVPRSSPDWACQQLSRNLCMLANNAHAPAGH----MNLRL----E 59
Db 14 VSLGLLVMTSAFPTPGPLGEDFKNDTPPSRLTLTPKTEALIKHIVDKISAIRKEICE 73
QY 60 EDE-----ETKNNVPRIQCEGCDPOGLKDNSQFCLORIROGLAFYKHLDD--SD 108
Db 74 KNDCEKSEKETAENKLLKLPKMEKDGCFQSGF--NQAICLIKTAGLLEQIYLDLQNL 131
QY 109 IFKGEFALLPDSPEQLHTSLGLSLQLQ-----PEDHPRETQOMPSLSSSQQWQR 159
Db 132 EPEGN-----QETVMELQSSIRTLQILKEKTAGLITTPATH---TDMLEKMOSSNEWVK 183
QY 160 PLRSKILRSQAFAIAAR 179
Db 184 NAKVVIILRSLENFLQFSRLR 203

RESULT 2
IL6_HORSE
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95181; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Horohov D.W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RT "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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DR EMBL; U64794; AAB87703.1; .
DR EMBL; AF005227; AAB62246.1; .
DR EMBL; AF041975; AAC04574.1; .
DR HSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 5 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> V (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 10.9%; Score 113; DB 1; Length 208;
Best Local Similarity 29.4%; Pred. No. 0.00092;
Matches 37; Conservative 22; Mismatches 51; Indels 16; Gaps 5;

QY 64 ETNNVPRIQCEGCDPOGLKDNSQFCLORIROGLAFYKHLDD--SDIFKGEFALLPDS 121
Db 84 ENNLNLPKMAEKDGFQSGF--NQETCLMKITTYGLSEFYLYLEVQLNEFKGKNIKTM- 140
QY 122 MEQLHTSLGLSLQLQPEDHPRETQOMPS-----LSSSQQWRPLLSKILRSQA 173
Db 141 --QISTKVL-VQILMQKNPEVTPDPTAKSLLAKLHSONEWLKNTHLLRSLEDF 197
QY 174 LAIAAR 179
Db 198 LQFSRLR 203

RESULT 3
IL6_CAPHI
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; Pubmed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells.";
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----  
 DR EMBL; X57317; CAA40572.1; -  
 DR PIR; S22162;  
 DR HSSP; P05231; IL16.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR InterPro; IPR003574; Interleukin\_6.  
 DR Pfam; PF00489; IL6; 1.  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR ProDom; PD004356; Interleukin\_6; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 1 29 BY SIMILARITY.  
 FT CHAIN 30 208 INTERLEUKIN-6.  
 FT DISULFID 72 78 BY SIMILARITY.  
 FT DISULFID 101 111 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 208 AA; 23758 MW; A0F000B9BA2EC341 CRC64;

Query Match 10.0%; Score 104; DB 1; Length 208;  
 Best Local Similarity 26.8%; Pred. No. 0.0067;  
 Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;  
 QY 59 EEDE-----ETKNVPRIQCDGCDPGQKDNQFCIQRIROGLAFYKHLDD--S 107  
 DB 73 EKNDCESSKETLAENKLNLPMEERKDCGQSGF--NQAICLIRTAGLEQVLDYDQ 130  
 QY 108 DIPKGPALLPSPMDQLHTSLGLSLLQLLOPE-----DHPRETQOMPSLSSQWQRP 161  
 DB 131 NEYGEQNVNRD-----LRKNITLIQILKQIKADIITPATNTDLLEKMQSSNEWVKN 185  
 QY 162 LRSKILRSIQAFIAAAR 179  
 DB 186 KIILRLNLENLFQFSLR 203

RESULT 6  
 IL6\_FELCA STANDARD; PRT; 208 AA.  
 AC F41683;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-6 precursor (IL-6).  
 GN IL6.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94162386; PubMed=8117820;  
 RA Onishi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,  
 RA Hasegawa A.;  
 RT "Molecular cloning of feline interleukin-6 cDNA.";  
 RL J. Vet. Med. Sci. 55:941-944(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocytes;  
 RX MEDLINE=94052249; PubMed=8234373;  
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;  
 RT "Molecular cloning and characterization of a cDNA encoding feline  
 interleukin-6.";  
 RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).  
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL  
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND  
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN  
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.  
 CC SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
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CC -----  
 DR EMBL; L16914; AAA16620.1; -  
 DR EMBL; D13227; BAA02507.1; -  
 DR HSSP; P05231; IL16.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR InterPro; IPR003574; Interleukin\_6.  
 DR Pfam; PF00489; IL6; 1.  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR ProDom; PD004356; Interleukin\_6; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 208 INTERLEUKIN-6.  
 FT DISULFID 68 74 BY SIMILARITY.  
 FT DISULFID 97 107 BY SIMILARITY.  
 FT CONFLICT 2 2 T -> N (IN REF. 2).  
 FT CONFLICT 45 45 S -> P (IN REF. 2).  
 FT CONFLICT 133 133 E -> K (IN REF. 2).  
 FT CONFLICT 173 187 AKLQSQEQLRHTTI -> LSCSHRRVAEAHNN (IN  
 FT REF. 2).  
 FT CONFLICT 200 201 FS -> LR (IN REF. 2).  
 SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match 9.9%; Score 103; DB 1; Length 208;  
 Best Local Similarity 24.8%; Pred. No. 0.0083;  
 Matches 38; Conservative 28; Mismatches 55; Indels 32; Gaps 6;  
 QY 52 GHMNLARE-----EDE-----ETKNVPRIQCDGCDPGQKDNQFCIQRIROGL 98  
 DB 58 GKISALKKCMCDNKNCKESKEALAEENLNLPKLAERKDCGQSGF--NQETCLTRITGL 115  
 QY 99 AFYKHLDD--SDIFKGPALLPDSPEQLHTSLGLSLLQLLOPEHPRETQOMP----- 149  
 DB 116 QEQIYLKFLQDKYEGD-----ENAKSVVTSTNVLLQMLKRGKNODEVTIPVPTVEVG 170  
 QY 150 ---SLSSSQWQRPRLRSKILRSIQAFIAAAR 179  
 DB 171 LQAKLQSQEQLRHTTIHLTLRLLEDFLQFSLR 203

RESULT 7  
 FSPB\_RAT STANDARD; PRT; 376 AA.  
 ID PSPB\_RAT  
 AC P22355;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pulmonary surfactant-associated protein B precursor (SP-B) (Pulmonary  
 DE surfactant-associated proteolipid SPL(Phe)).  
 GN SFTPB OR SFTP3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89150284; PubMed=2920185;  
 RA Emrie P.A., Shannon J.M., Mason R.J., Fisher J.H.;  
 RT "cDNA and deduced amino acid sequence for the rat hydrophobic

RT pulmonary surfactant-associated protein, SP-B.";  
 RL Biochim. Biophys. Acta 994:215-221(1989).  
 CC -!- FUNCTION: PULMONARY SURFACTANT-ASSOCIATED PROTEINS PROMOTE  
 CC ALVEOLAR STABILITY BY LOWERING THE AIR-FLUID TENSION AT THE AIR-  
 CC LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES  
 CC THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINewTONS  
 CC PER METER.  
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%  
 CC PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,  
 CC CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL  
 CC HYDROPHOBIC PROTEINS (SP-B AND SP-C).  
 CC -!- SIMILARITY: CONTAINS 1 SAPOSIN A-TYPE DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 3 SAPOSIN B-TYPE DOMAINS.  
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 CC -----  
 DR EMBL; X14778; CAA32885.1; -.  
 DR PIR; S02766; S02766.  
 DR HGSP; P07988; IDFW.  
 DR InterPro; IPR003119; SapA.  
 DR InterPro; IPR000004; SapB.  
 DR InterPro; IPR003258; Surfactant\_B.  
 DR Pfam; PF02199; SAPA; 1.  
 DR Pfam; PF03489; Surfactant\_B; 1.  
 DR ProDom; PD001732; SapB; 1.  
 DR ProDom; PD008002; Surfactant\_B; 1.  
 DR SMART; SM00162; SAPA; 1.  
 DR SMART; SM00118; SAPB; 3.  
 DR Surface film; Gaseous exchange; Glycoprotein; Repeat.  
 KW PROPEP 1 190  
 FT CHAIN 191 269 PULMONARY SURFACTANT-ASSOCIATED PROTEIN  
 FT B.  
 FT PROPEP 270 376  
 FT DOMAIN 26 59  
 FT DISULFID 198 267 SAPOSIN-LIKE TYPE A.  
 FT DISULFID 201 261 BY SIMILARITY.  
 FT DISULFID 225 236 BY SIMILARITY.  
 FT DISULFID 238 238 BY SIMILARITY.  
 FT CARBOHYD 306 306 INTERCHAIN (BY SIMILARITY).  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 376 AA; 41590 MW; F329DCG2E73FB4C CRC64;

Query Match 9.8%; Score 101.5; DB 1; Length 376;  
 Best Local Similarity 29.3%; Pred. No. 0.024; Mismatches 70; Indels 41; Gaps 11;  
 Matches 55; Conservative 22;  
 QY 10 LLLLPVY-TGLAVPRSSPDMAQ-----CQQLSRNL-----CMLANNAHAPAGHM-- 54  
 Db 9 LLLLPVY-TGLAVPRSSPDMAQ-----CQQLSRNL-----CMLANNAHAPAGHM-- 54  
 QY 55 -----NLLREEDEETKNVPRIOEDGCDPGLKDNQSGFCLQRIQGLAFLYKHLSD 108  
 Db 69 ECEDIIVHLTKMTKTFDAFQDTIRKFLQEQCDLPLV-----LLVPRCRQVLDVPLV-ID 123  
 QY 109 IFKGEFALLPDSPEQHLTSLGLQLQLQEDHPHRETQOMPSSLSQQWQRPILRSKILR 168  
 Db 124 YFGQ--IKPKAICS--HVGLCLPLGQ-TRPEQKPEMLDAIPN-----PLLNLKVLVP 169  
 QY 169 SLQ-AFLA 175  
 Db 170 ALPCAFLA 177  
 RESULT 8  
 ID IL6\_PIG STANDARD; PRT; 212 AA.

AC P26893; Q95KN6;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-6 precursor (IL-6).  
 GN IL6.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91338547; PubMed=1873476;  
 RA Richards C., Saklatvala J.;  
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and  
 RL expression of mRNA in synovial fibroblasts in vitro.";  
 RL Cytokine 3:269-276(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92360284; PubMed=1497880;  
 RA Mathialagan N., Bixby J.A., Roberts M.R.;  
 RT "Expression of Interleukin-6 in porcine, ovine, and bovine  
 RL preimplantation conceptuses".  
 RL Mol. Reprod. Dev. 32:324-330(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Landrace x Meishan; TISSUE=Blood;  
 RA Liu S., Meng M., Gao R.;  
 RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan  
 RL hybrid swine.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL  
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION  
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND  
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN  
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
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 CC -----  
 DR EMBL; M86722; AAC37333.1; -.  
 DR EMBL; M80258; AAC27127.1; -.  
 DR EMBL; AF309651; AAG27730.1; -.  
 DR HSSP; P05231; IALU.  
 DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
 DR InterPro; IPR003574; Interleukin\_6.  
 DR Pfam; PF00489; IL6; 1.  
 DR PRINTS; PR00433; IL6GCSFMGF.  
 DR ProDom; PD004356; Interleukin\_6; 1.  
 DR SMART; SM00126; IL6; 1.  
 DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Signal.  
 FT SIGNAL 1 29 BY SIMILARITY.  
 FT CHAIN 30 212 INTERLEUKIN-6.  
 FT DISULFID 72 78 BY SIMILARITY.  
 FT DISULFID 101 111 BY SIMILARITY.  
 FT CONFLICT 30 30 E -> G (IN REF. 1).  
 SQ SEQUENCE 212 AA; 23952 MW; 1E736FB230BAFC5D CRC64;

Query Match 9.6%; Score 100; DB 1; Length 212;  
 Best Local Similarity 25.0%; Pred. No. 0.016;  
 Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps 5;  
 QY 52 GHMNLREEDE-----ETKNVPRIOEDGCDPGLKDNQSGFCLQRIQGL 98  
 Db 62 KGISAMRKEMCEKYEKCNSEKVENNLPKMAEKDGCFCQSGF--NQETCLMRITTL 119



```
RL Eur. J. Biochem. 176:187-197(1988).
RN [8]
RP SEQUENCE OF 66-75; 78-84 AND 128-148.
RX MEDLINE=90147691; PubMed=2302197;
RA Jahn W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
RT "Internal amino acid sequencing of proteins by in situ cyanogen
RT bromide cleavage in polyacrylamide gels.";
RL Biochem. Biophys. Res. Commun. 166:139-145(1990).
RN [9]
RP SEQUENCE OF 25-45.
RX MEDLINE=87092311; PubMed=2948184;
RA van Snick J., Cayphas S., Vink A., Uyttenhove C., Coullie P.G.,
RA Rubira M.R., Simpson R.J.;
RT "Purification and NH2-terminal amino acid sequence of a
RT T-cell-derived lymphokine with growth factor activity for B-cell
RT hybridomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; X06203; CAA29560.1; -
DR EMBL; M20572; AAA39302.1; -
DR EMBL; X51457; CAA35824.1; -
DR EMBL; J03783; AAA39301.1; -
DR EMBL; X54542; CAA38411.1; -
DR EMBL; M24221; AAA68814.1; -
DR EMBL; A30531; ICM56.
DR HSP; P05231; IALU.
DR MGD; MGI:96559; IL6.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24384 MW; BBB47DDA9E86787A CRC64;

Query Match 9.2%; Score 96; DB 1; Length 211;
Best Local Similarity 25.5%; Pred. No. 0.04;
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGDCDPQGLKDNQSQCLO 92
DB 64 EMRKELC-----NGNSDC--MN-----NDALAENNLKLPQLRNDGGCYQTGY--NQEICLL 111
QY 93 RIRQGLAFYKHLID-----SDIFKEPALLP-----DSPMEQHLTSL--GLSQ 134
DB 112 KISSGLLEHVSLEYLKMKNLKNKKDKARVLQRTDTETLHIFNQEVKDLKIVLPTPIGN 171
QY 135 LIQPEDHPRETQMPSSLSSQOWORPLLRSKILRSLOAFATAAR 179
DB 172 ALLTD-----KLESQKELWRTKTIQFIKLSLEEFKVTLR 206
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RESULT 11
IL6_RAT
ID IL6_RAT STANDARD; PRT; 211 AA.
AC P20607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89380206; PubMed=2789217;
RA Northemann W., Braciak T.A., Hattori M., Lee F., Fey G.H.;
RT "Structure of the rat interleukin 6 gene and its expression in
RT macrophage-derived cells.";
RL J. Biol. Chem. 264:16073-16082(1989).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; M26744; AAA77659.1; -
DR EMBL; M26745; AAA41430.1; -
DR PIR; A34247; A34247.
DR HSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 8.8%; Score 91; DB 1; Length 211;
Best Local Similarity 24.5%; Pred. No. 0.12;
Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGDCDPQGLKDNQSQCLO 92
DB 64 EMRKELC-----NGNSDC--MN-----SDALSENKLPQLRNDGGCYQTGY--NOEICLL 111
QY 93 RIRQGLAFYKHLID-----SDIFKEPALLP-----DSPMEQHLTSL--GLSQ 143
DB 112 KISSGLLEHVSLEYLKMKNLKNKKDKARVLQRTDTETLHIFNQEVKDLKIVLPTPIGN 167
QY 144 ETQQ---NPSLSSQOWORPLLRSKILRSLOAFATAAR 179
DB 168 PTSNALLMEKLESQKWLRTKTIQFIKLSLEEFKVTMR 206

RESULT 12
IL6_PHOVI
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ID IL6_PHOVI STANDARD; PRT; 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel D.A., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick M.B.
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; L46802; AAB01430.1; -
DR HSSP; P05231; 1IL6.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR KEGG; Glycopolin; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL <1 26 BY SIMILARITY.
FT CHAIN 27 209 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
SQ SEQUENCE 209 AA; 23483 MW; 75144922E43B48E9 CRC64;
Query Match 8.7%; Score 90; DB 1; Length 209;
Best Local Similarity 27.3%; Pred. No. 0.15;
Matches 42; Conservative 25; Mismatches 53; Indels 34; Gaps 10;
QY 52 GHMNLREE-----EDEE---TKNN---VPRIQEDGCDPQGLKDNQSQFCLQRIQG- 97
Db 59 KTSIALKEMCDKYNKNCDSKEALNRLPKLAEKDGFQSGF--NOETCLTRITGL 116
QY 98 LAFYKHU--LDSDIFGEPALLPSPMEQLHTSLGLSLLQLLQPE-----DHPRET 145
Db 117 LEFQHLKLYIQAN-YEGNK---EDANSVYISTKL--LVQMLMKVKKSQDEVTPDPTTDT 170
QY 146 QQPSLSSSQWQORPLRLSKILRSLOAFIAAAR 179
Db 171 SLQAILKAQDKWLKHTTHILKLSLEDFLQFSLR 204
RESULT 13
FRZ3_DROME
ID FRZ3_DROME, STANDARD; PRT; 581 AA.
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AC O77438; Q91727; Q9NIU0; Q9U902; Q9W5D5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled protein 3 precursor (Frizzled-3) (DFz3).
GN FZ3 OR EG:34F3.6 OR CG16785.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; PubMed=10498678;
RA Sato A., Kojima T., Ui-Tei K., Miyata Y., Saigo K.;
RT "Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
RT of Wingless signaling in wingless hypomorphic mutants.";
RL Development 126:4421-4430(1999).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=20171076; PubMed=10704878;
RA Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The Wingless target gene Dfz3 encodes a new member of the Drosophila
RT Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
RN [3]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX STRAIN-Oregon-R;
MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlancourt A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valentini P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
RN [4]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX STRAIN-Berkeley;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
```

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swlrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -|- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors  
 CC are coupled to the beta-catenin canonical signaling pathway, which  
 CC leads to the activation of dishevelled proteins, inhibition of  
 CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation  
 CC of Wnt target genes. A second signaling pathway involving PKC and  
 CC calcium fluxes has been seen for some family members, but it is  
 CC not yet clear if it represents a distinct pathway or if it can be  
 CC integrated in the canonical pathway, as PKC seems to be required  
 CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem  
 CC to involve interactions with G-proteins. Required to coordinate  
 CC the cytoskeletons of epidermal cells to produce a parallel array  
 CC of cuticular hairs and bristles.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -|- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a  
 CC short form; are produced by alternative splicing.  
 CC -|- TISSUE SPECIFICITY: Wing, leg and eye imaginal disks. In embryos,  
 CC expressed is seen in brain, proventriculus, Malpighian tubules,  
 CC anal plate and visceral mesoderm of parasegment 8.  
 CC -|- DEVELOPMENTAL STAGE: Expressed in embryos from stage 11 and in  
 CC larvae.  
 CC -|- DOMAIN: The fz domain is involved in binding with Wnt ligands (By  
 CC similarity).  
 CC -|- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED  
 CC RECEPTORS.  
 CC -|- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.  
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 DR EMBL; AR018565; BAA84677.1; -;  
 DR EMBL; AF195242; AAF63250.1; -;  
 DR EMBL; AL031583; CAA20896.1; -;  
 DR EMBL; AF003418; AAF45547.1; -;  
 DR EMBL; AF003418; AAG22363.1; -;  
 DR FlyBase; FBgn0027343; fz3  
 DR InterPro; IPR000539; Frizzled.  
 DR InterPro; IPR000024; Fz\_domain.  
 DR Pfam; PF01534; Frizzled; 2.  
 DR Pfam; PF01392; Fz; 1.  
 DR PRINTS; PR00489; FRIZZLED.  
 DR SMART; SM00063; FRI; 1.  
 DR PROSITE; PS50038; FZ; 1.  
 DR PROSITE; PS50261; G-PROTEIN\_RECEP\_F2\_4; 1.  
 DR Multigene family; Receptor; G-protein coupled receptor; Transmembrane;  
 KW Developmental protein; Glycoprotein; signal; Alternative splicing.  
 FT SIGNAL 1 19 POTENTIAL  
 FT CHAIN 20 581 FRIZZLED PROTEIN 3.  
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 1 (POTENTIAL).  
 FT DOMAIN 259 270 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 271 291 2 (POTENTIAL).  
 FT DOMAIN 292 321 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 322 342 3 (POTENTIAL).  
 FT DOMAIN 343 359 4 (POTENTIAL).  
 FT TRANSMEM 360 380 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 394 414 5 (POTENTIAL).  
 FT DOMAIN 415 442 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 443 463 6 (POTENTIAL).  
 FT DOMAIN 464 488 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 489 509 7 (POTENTIAL).  
 FT DOMAIN 510 581 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 581 581 7 (POTENTIAL).  
 FT SITE 581 581 POLY-LEU.  
 FT CARBOHYD 581 581 PDZ-BINDING.  
 FT CARBOHYD 581 581 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 581 581 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARSPLIC 581 581 MISSING (IN SHORT ISOFORM).  
 FT VARSPLIC 581 581 TALPNLGHNTQLAEQL -> MDKTKKRCVGLDYLIP  
 FT VARSPLIC 581 581 (IN SHORT ISOFORM).  
 FT CONFLICT 581 581 T -> I (IN REF. 1).  
 FT CONFLICT 192 192 A -> V (IN REF. 1).  
 FT CONFLICT 276 276 L -> P (IN REF. 1).  
 FT CONFLICT 304 304 G -> W (IN REF. 4).  
 FT CONFLICT 376 376 A -> V (IN REF. 1).  
 SQ SEQUENCE 581 AA; 63251 MW; 07A8BBFF2A9E3F93 CRC64;  
 Query Match 8.6%; Score 89.5; DB 1; Length 581;  
 Best Local Similarity 29.0%; Pred. No. 0.59;  
 Matches 45; Conservative 23; Mismatches 60; Indels 27; Gaps 10;  
 QY 6 AVIMLWLLPWTQGLA-----VPRSSPDWAQCOQLSRNLCM-LAWNAHA---PAG 52  
 Db 4 ASILLHLTWAVATIAANGAGHGPVAGCPNGLQCCQGLGYNTALPNLJAG 63  
 QY 53 HMNLLREDEETKNNVPRIQCDCDPQG--LKDNSOF--CLQIRIQLGLAFYKHLSD 108  
 Db 64 HTNQL--EAELQIAKLVLPLI--ESGCSRRARFLLCSSLFPLCTPDVPRPVAACKLLET- 118  
 QY 109 IFKGPALLPSPME--QLHTSLILGLSOLLQPEDH 141  
 Db 119 -VRGE--CMENAPPELMELWPSFLNCDGLPQPEKH 150  
 RESULT 14  
 ID NH20\_CAEEL STANDARD; PRT; 457 AA.  
 AC Q09565; G9GTI6;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nuclear hormone receptor family member nhr-20.  
 GN NHR-20 OR F43C1.4.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peioderinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Jessal B., Smith A.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP REVISIONS.  
 RA Durbin R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 4-457 FROM N.A.  
 RA Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;  
 RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical  
 RL compatibility with the ligand-binding domain fold".  
 CC Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: ORPHAN NUCLEAR RECEPTOR.  
 CC -|- SUBCELLULAR LOCATION: Nuclear (potential).  
 CC -|- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:20 ; Search time 26.9818 Seconds  
(without alignments)  
1496.757 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLCRAVIMLWLPWVTQGL.....AARVFAHGAATLPELVPTA 196

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1038	100.0	196	11 Q9EQ14	Q9eq14 mus musculus
2	915	88.2	196	11 Q91Z84	Q91z84 rattus norv
3	718.5	69.2	189	4 Q9H2A5	Q9h2a5 homo sapien
4	717.5	69.1	189	4 Q9NPF7	Q9npf7 homo sapien
5	663.5	63.9	193	6 Q9N2H9	Q9n2h9 sus scrofa
6	113.5	10.9	208	6 Q9XT80	Q9xt80 delphinapte
7	106	10.2	207	6 Q9MYZ7	Q9myz7 canis famli
8	98	9.4	212	11 Q91ZL3	Q91zl3 sigmodon hi
9	95	9.2	210	11 Q9WVQ8	Q9wvq8 mesocricetu
10	91	8.8	209	6 Q9TTH3	Q9tth3 aotus lemur
11	90	8.7	241	6 Q9MZR1	Q9mzr1 oryctolagus
12	89.5	8.6	1217	10 Q94I37	Q94i37 oryza sativ
13	89	8.6	4306	11 Q9J7J9	Q9j7j9 rattus norv
14	86.5	8.3	195	6 Q9GJU0	Q9gju0 felis silve
15	86.5	8.3	353	10 Q9SX30	Q9sxx30 arabidopsis
16	86.5	8.3	354	10 Q9VZS3	Q9vzs3 arabidopsis

17	84.5	8.1	432	10 Q9FHP0	Q9fhp0 arabidopsis
18	84.5	8.1	1026	10 Q49529	Q49529 arabidopsis
19	84	8.1	209	6 Q97540	Q97540 aotus nancy
20	83	8.0	207	6 Q28403	Q28403 enhydra lut
21	83	8.0	508	5 Q8T012	Q8t012 drosophila
22	83	8.0	531	16 Q92281	Q92281 rhizobium m
23	83	8.0	857	5 Q9V624	Q9v624 drosophila
24	82.5	7.9	293	16 Q9HV75	Q9hv75 pseudomonas
25	82	7.9	708	4 Q96A93	Q96a93 homo sapien
26	82	7.9	712	4 Q8TEY4	Q8tey4 homo sapien
27	81	7.8	652	5 Q77168	Q77168 apis mellif
28	80.5	7.8	241	13 Q90Y10	Q90y10 gallus gall
29	80.5	7.8	962	5 Q9U552	Q9u552 caenorhabdi
30	80	7.7	603	16 Q8XXA0	Q8xxa0 talstonia s
31	80	7.7	1011	4 Q9H0F4	Q9h0f4 homo sapien
32	80	7.7	1731	4 Q8TEP8	Q8tep8 homo sapien
33	79.5	7.7	953	2 Q9L4W0	Q9l4w0 streptomyce
34	79.5	7.7	6875	6 Q28733	Q28733 oryctolagus
35	79	7.6	108	6 Q9BDL5	Q9bdl5 phocoenoide
36	79	7.6	557	11 Q91WJ7	Q91wj7 mus musculu
37	79	7.6	558	11 Q8VC37	Q8vc37 mus muscul
38	79	7.6	605	2 Q8VT81	Q8vt81 agrobacteri
39	79	7.6	1833	5 Q95ZU1	Q95zu1 caenorhabdi
40	79	7.6	1835	5 Q95ZU2	Q95zu2 caenorhabdi
41	79	7.6	1839	5 Q17383	Q17383 caenorhabdi
42	78.5	7.6	207	11 Q9JHH3	Q9jhh3 marmota mon
43	78.5	7.6	530	10 Q9C9S0	Q9c9s0 arabidopsis
44	78.5	7.6	797	16 Q8YJB8	Q8yjb8 bruceella me
45	78	7.5	285	16 Q9I649	Q9i649 pseudomonas

## ALIGNMENTS

RESULT 1  
Q9EQ14  
ID Q9EQ14 PRELIMINARY; PRT; 196 AA.  
AC Q9EQ14;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Interleukin 23 p19 subunit (Interleukin 23, alpha subunit p19).  
GN IL23A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20567322; PubMed=11114383;  
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,  
Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,  
Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,  
Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,  
Kastelein R.A.;  
RT "Novel p19 Protein Engages IL-12p40 to Form a Cytokine, IL-23, with  
Biological Activities Similar as Well as Distinct from IL-12";  
RL Immunity 13:715-725(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RP Strausberg R.;  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF301619; AAC37231.1; -;  
DR EMBL; BC019953; AAH19953.1; -;  
DR MGD; MGI:1932410; IL23a.  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR SMART; SM00126; IL6; 1  
SQ SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;

Query Match 100.0%; Score 1038; DB 11; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2e-101;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 180
|||
QY 181 FAHGAATLTPVPTA 196
|||
DB 181 FAHGAATLTPVPTA 196
|||
RESULT 2
Q91284 PRELIMINARY; PRT; 196 AA.
AC Q91284;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Interleukin 23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.
RA Tran G., Hodgkinson S.;
RT "Rattus norvegicus il-23 mRNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055379; AAL18229.1; -.
SQ SEQUENCE 196 AA; 21986 MW; 188FF74BC409A961 CRC64;

Query Match 88.2%; Score 915; DB 11; Length 196;
Best Local Similarity 87.8%; Pred. No. 1.9e-88;
Matches 172; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 180
|||
QY 181 FAHGAATLTPVPTA 196
|||
DB 181 FAHGAATLTPVPTA 196
|||
RESULT 3
Q9H2A5 PRELIMINARY; PRT; 189 AA.
AC Q9H2A5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin 23 p19 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=20567322; PubMed=11114383;
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
RA Yu N., Wang J., Singh K., Zonin F., Vaishberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with
RT Biological Activities Similar as Well as Distinct from IL-12.";
RL Immunity 13:715-725(2000).
DR EMBL; AF301620; AAG37232.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 189 AA; 20744 MW; BFB5C0F42D4CIE3A CRC64;

Query Match 69.2%; Score 718.5; DB 4; Length 189;
Best Local Similarity 74.6%; Pred. No. 9.3e-68;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 59
|||
QY 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 119
|||
QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQOWORPLRLSKILRSLOAFLAIAARV 179
|||
QY 181 FAHGAATLTPVPTA 189
|||
DB 181 FAHGAATLTPVPTA 188
|||
RESULT 4
Q9NPF7 PRELIMINARY; PRT; 189 AA.
AC Q9NPF7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SGRF precursor.
DE SGRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Hirata Y., Kosuge Y.;
RT "SGRF: a novel member of the IL-6/G-CSF family.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030000; BAA93886.1; -.
DR EMBL; AB030001; BAA93687.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
KW Signal.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 189 SGRF.
SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;

Query Match 69.1%; Score 717.5; DB 4; Length 189;
Best Local Similarity 74.6%; Pred. No. 1.2e-67;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 59
|||
QY 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGDCDPOGLKDNSQFCQRIROGLAFYKHLSDIFKGEPAALLPDS 120
|||
QY 181 FAHGAATLTPVPTA 189
|||
DB 181 FAHGAATLTPVPTA 188
|||
```





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[2]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Palmer L.E., Bal H., Spiegel L.A., Huang E.N., Rodriguez M.A.,
de la Bastide M., Preston R.R., Nascimento L.U., King L., Shah R.S.,
Kirchoff K.A., Vli M.D., Baker J.P., Miller B., Toth K., Shah R.S.,
O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Palmer L.E., Bal H., Spiegel L.A., Huang E.N., Rodriguez M.A.,
de la Bastide M., Preston R.R., Nascimento L.U., King L., Shah R.S.,
O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC021891; AAK50412.1; -
DR InterPro; IPR001584; Rve.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00655; rve.1
DR Pfam; PF000986; zf-CCHC; 1
SQ SEQUENCE 1217 AA; 134726 MW; 36B9BD25FE629743 CRC64;

Query Match      8.6%; Score 89.5; DB 10; Length 1217;
Best Local Similarity 28.2%; Pred. No. 1.9;
Matches 37; Conservative 20; Mismatches 37; Indels 37; Gaps

QY 14 PWTQGLAVPRSSPDWAQCOOLSRNICML-----AWNHAHAPAGHMNL--LREEDEEET 65
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 448 PW-LVMKVRRTSNLYRIEQLQASQVCLASLDNPAWLHARIGHVFNHAKLLVVKEM 506
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 66 KNNVPRIOCEDCGDPOGLKDNSQCL--QRQQ---GLAFYKHLSDIFKGEFALLPDS 120
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 507 ASGVPTVH-----HPNQL--CQACLVAKQVRQPFPGMANYR-----AEA 543
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 121 PMEQLHTSLLG 131
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 544 PLELHMDLGC 554

RESULT 13
ID J9J9 PRELIMINARY; PRT; 4306 AA.
AC Q9J979;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytoplasmic dynein heavy chain.
GN DNCHC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus
OX NCBI_TaxID=10116;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Mikami A.;
RA Mikami A.;
RT "Molecular analysis of cytoplasmic dynein.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Mikami A., Vallee R.B.;
RT "In vitro expression of enzymatically active cytoplasmic dynein heavy
chain fragments.";
RL Mol. Biol. Cell 9:276-276(1998).
DR EMBL; AB041881; BAA97048.1; -
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
SQ SEQUENCE 4306 AA; 492206 MW; A4AC9B7B9E7FA330 CRC64;

```

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Query Match      8.6%; Score 89; DB 11; Length 4306;
Best Local Similarity 28.0%; Pred. No. 10;
Matches 40; Conservative 20; Mismatches 55; Indels 28; Gaps 8;

QY 53 HNNLREDEETKNNPRIQEDCGDPOGLKDNSQFCL--QRIROGLAFYKHLSDS-- 108
Db 20 YFGLRPELMDQTPLSNCPVW-----NFLDDGNQMLLRVORS DAGLAF-SNTIDFDDT 71

QY 109 -----IFKGEFALLPDSPEQLHTSLGLSOLLQPEDHPRETOOM---PSLSSSQWQR 159
Db 72 KDKVLVFFKLRPEVITDG---NLHTNILVSSMLESPINSLYQAVQVFPAPMLLKQDEWSR 128

QY 160 ---PLRSKILRSLOAFIAIAR 179
Db 129 NFDPKLQN-LLSELAGLVLR 150

RESULT 14
Q9GUUO
ID Q9GUUO PRELIMINARY; PRT; 195 AA.
AC Q9GUUO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN G-CSF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RA Yamanoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,
RA Tsuchimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Yamanoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RA Tsuchimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042552; BAB17789.1; -.
DR EMBL; AB042553; BAB17757.1; -.
DR HSSP; P35834; 1BGE.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 21 POTENTIAL.
Query Match      8.3%; Score 86.5; DB 6; Length 195;
Best Local Similarity 28.3%; Pred. No. 0.4;
Matches 34; Conservative 20; Mismatches 51; Indels 15; Gaps 5;

QY 78 CDPQGLKDNSQFCLQRIROGLAFYKHLSDIFKGEFALLPDSPEQLHTSLGLSOLLQ 137
Db 85 CSSQALQITG--CLRLQHSGLFYQGLLQA-LAGISPELAPTLDMQLQDITDFAINIQW 141

QY 138 PED-----HPRETOQMPSSLSSSQWQRPLRSKILRSLOAFIAIARVFAHCAATLTP 191
Db 142 MEDYGMAPVPPQTGTMTFTA--FORRAGGTLVASNLQSFLEVAYRALRH-----FTKP 195

RESULT 15
Q9SX30
ID Q9SX30 PRELIMINARY; PRT; 353 AA.
AC Q9SX30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE F24J5.9.
GN F24J5.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RA STRAIN=CV. COLOMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Gonzalez A., Liu A., Vaysberg M., Sakano H.,
RA Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008075; AAD49976.1; -.
SQ SEQUENCE 353 AA; 39293 MW; DE6DCDAFC6EC4A0C CRC64;

Query Match      8.3%; Score 86.5; DB 10; Length 353;
Best Local Similarity 26.2%; Pred. No. 0.84;
Matches 43; Conservative 20; Mismatches 48; Indels 53; Gaps 9;

QY 26 SSP-----DWAQCOQLSRNLCMLAWNAHAPAGHMNLLREEDEETKNNVPRIOCEDG 77
Db 104 SSPELVNNKSDWLSVQL-----WN-HSP-----DLNPKERVAKKAKVVEVKPSG 150

QY 78 C-DPQGLKDNSQFCLQRIROGLAFYKHLSDIFKGEFALLPDSPEQLHTSL--G 131
Db 151 AFQP-----FQKRVLETDL---QPAVKVASSMPATTTSTTETCGG 188

QY 132 LSQQLQPEDHPRETOQMPSSLSSSQWQR---PLRSKILRSLO 171
Db 189 KSDLIKAGDEERRIEQQSQSOSHTHRKQRRCWSPELHRRFLNALQ 232

Search completed: November 20, 2002, 11:54:26
Job time : 28.9818 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:39 ; Search time 33.6 seconds  
(without alignments)  
777.295 Million cell updates/sec

Title: US-09-658-699-4

Perfect score: 1038

Sequence: 1 MLCGRAVIMLWLLPWVTQGL.....AARVFAHGAATTEPLVPTA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_101002.\*

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2:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1038	100.0	196	20 AAY29784	Mouse interleukin
2	1038	100.0	196	20 AAW95003	Mouse interleukin
3	1038	100.0	196	21 AAB01982	Murine interleukin
4	1038	100.0	196	22 AAB47121	Murine IL-B30. Mu
5	718.5	69.2	189	20 AAY29783	Human interleukin
6	718.5	69.2	189	20 AAW95002	Human interleukin
7	718.5	69.2	189	21 AAB01981	Human interleukin
8	718.5	69.2	189	22 AAB47120	Human IL-B30. Hom
9	717.5	69.1	189	21 AAY94966	Human secreted pro
10	717.5	69.1	189	21 AAY54606	SGRF protein seque

11	717.5	69.1	189	22 AAU12287	Human PR05798 poly
12	717.5	69.1	189	22 AAB48070	Human extracellular
13	356	34.3	102	20 AAY29787	Partial pig interl
14	356	34.3	102	20 AAW95004	Pig interleukin-B3
15	356	34.3	102	21 AAB01983	Mature porcine int
16	115	11.1	208	13 AAR22125	Sequence of ovine
17	112	10.8	181	13 AAR22128	Sequence of ovine
18	112	10.8	184	20 AAW95012	Sheep interleukin
19	104	10.0	208	22 AAB99342	Bovine interleukin
20	96	9.2	188	20 AAB95013	Mouse interleukin
21	96	9.2	211	14 AAR33385	Cytokine mIL-6. M
22	96	9.2	211	15 AAB49040	Murine interleukin
23	92.5	8.9	186	14 AAR31997	Met-IL-6 SSCC mute
24	92.5	8.9	186	15 AAR72212	Human interleukin
25	92.5	8.9	186	17 AAW05587	SSCC mutein of hum
26	91	8.8	211	11 AAR06847	Rat interleukin-6
27	89.5	8.6	581	22 ABB68074	Drosophila melanog
28	89	8.6	212	14 AAR33384	Cytokine hIL-6. H
29	89	8.6	212	22 AAB49786	Human interferon b
30	88	8.5	181	22 AAU16191	Human novel seque
31	88	8.5	181	22 AAU16606	Segment of B-cell
32	88	8.5	185	11 AAR05311	Full length interl
33	88	8.5	185	15 AAR45718	Human mutant IL-6a
34	87.5	8.4	162	16 AAR77391	Human interleukin
35	87.5	8.4	163	17 AAW00132	Human IL-6 mutant
36	87.5	8.4	177	16 AAR77388	Human interleukin
37	86.5	8.3	162	17 AAW00131	Human interleukin
38	86.5	8.3	174	20 AAW95006	Feline G-CSF seque
39	86.5	8.3	195	20 AAY02471	A granulocyte colo
40	86.5	8.3	309	22 ABG15321	Novel human diagno
41	86.5	8.3	319	16 AAR80147	Chimeric interleuk
42	86.5	8.3	337	16 AAR79324	IL-3 containing fu
43	86.5	8.3	337	21 AAY53205	Human interleukin
44	86.5	8.3	337	22 AAE13999	Myelopietin (MPO)
45	86.5	8.3	347	19 AAW78103	Chimeric receptor

#### ALIGNMENTS

#### RESULT 1

AA29784  
ID AAY29784 standard; Protein; 196 AA.

XX AC

XX AC

DT 04-NOV-1999 (first entry)

XX AC

XX AC

DE Mouse interleukin B30.

XX AC

XX AC

KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;

KW interleukin B30; DSR1; DCRL1; IL-B30; cytokine receptor; diagnosis;

KW inflammatory disorder; inflammatory response; innate immunity;

KW morphogenic development; immunological disorder.

XX Mus sp.

OS Mus sp.

XX Key

XX Key

FT Peptide

FT Peptide

FT Protein

FT Protein

FT /label= IL-B30

XX WO9940195-A1.

PN Mouse interleukin

XX 12-AUG-1999.

XX 05-FEB-1999;

XX 99WO-US02600.

PR 13-MAY-1998;

PR 06-FEB-1998;

XX 98US-0078194.

XX 98US-0073941.

PA (SCHE ) SCHERING CORP.

```

XX Kastelein RA; Mattson JD, McClanahan TK;
PI
XX WPI; 1999-527306/44.
DR N-PSDB; AAZ08866.
XX
PT New receptor subunits useful in the treatment inflammatory disorders
XX
PT Claim 2; Page 27-28; 133pp; English.
XX
XX The present invention describes a composition (I) comprising DNAX
CC cytokine receptor subunit I (DCSR1) protein and DNAX soluble receptor
CC subunit I (DSRS1) protein, which together encode a new mammalian
CC cytokine-related receptor (R), or DCSR1 and interleukin B30 (IL-B30)
CC proteins, or DSRS1 and IL-B30 proteins. (I) comprising DSRS1 and DCSR1
CC is useful for screening for ligands (i.e. agonists/antagonists) from
CC a library of compounds, which are useful for modulating the physiology
CC or development of a cell or tissue culture e.g. inflammatory responses,
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal expression of
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC and the subunits DSRS1 and DCSR1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the specifically claimed mouse IL-B30, for use in the
CC composition of the present invention.
XX
XX Sequence 196 AA;
SQ
Query Match 100.0%; Score 1038; DB 20; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.2e-99;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHNNLLREE 60
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHNNLLREE 60
QY 61 EDEETKNNVPRIQCEDCGDPQGLKDNSQFCQRIQROGLAFYKHLSDIFKGEPAALLPDS 120
DB 61 EDEETKNNVPRIQCEDCGDPQGLKDNSQFCQRIQROGLAFYKHLSDIFKGEPAALLPDS 120
QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQWQORPLLRSKILRSLOAFLAIAARV 180
DB 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQWQORPLLRSKILRSLOAFLAIAARV 180
QY 181 FAHGAATLTPELVPTA 196
DB 181 FAHGAATLTPELVPTA 196
RESULT 2
AAW95003
ID AAW95003 standard; Protein; 196 AA.
XX
XX AAW95003;
AC
XX
XX 21-MAY-1999 (first entry)
DT
XX
XX Mouse interleukin-B30 (IL-B30) polypeptide.
DE
XX
XX Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
KW inflammatory condition; drug screening; mouse.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 1..21
FT Peptide /note= "signal peptide"
FT 22..196
FT Protein /note= "mature protein"
XX
XX

```

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PN WO9905280-A1.
XX
XX 04-FEB-1999.
XX
XX 24-JUL-1998; 98WO-US15423.
XX
XX 25-JUL-1997; 97US-0900905.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Bazan JF;
PI
XX WPI; 1999-142935/12.
DR N-PSDB; AAX17787.
XX
XX Newly isolated or recombinant polynucleotide encoding mammalian
PT cytokine interleukin-B30 (IL-B30), including fragments - useful for
PT regulating activation, development, differentiation and function of
PT various cell types, and for diagnosing and treating conditions
PT associated with IL-B30
XX
XX Claim 2; Page 9-10; 83pp; English.
XX
XX This represents a mouse cytokine interleukin-B30 (IL-B30) polypeptide.
CC Host cells containing a vector comprising the IL-B30 nucleic acid are
CC used for the recombinant production of the protein. The polynucleotides
CC are useful for diagnosis of IL-B30 mediated conditions, and forensic
CC science (e.g. to distinguish rodent from human, or as a marker to
CC distinguish between different cells exhibiting differential expression or
CC modification patterns). The IL-B30 (including fragments), together with
CC antibodies that bind to IL-B30 are useful for teaching purposes. They
CC are also used for treating conditions associated with abnormal physiology
CC or development, including inflammatory conditions. The polypeptide
CC cytokine should mediate cytokine synthesis and proliferation in cells.
CC IL-B30 is useful for drug screening to identify compounds having binding
CC affinity to IL-B30.
XX
XX Sequence 196 AA;
SQ
Query Match 100.0%; Score 1038; DB 20; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.2e-99;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHNNLLREE 60
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHNNLLREE 60
QY 61 EDEETKNNVPRIQCEDCGDPQGLKDNSQFCQRIQROGLAFYKHLSDIFKGEPAALLPDS 120
DB 61 EDEETKNNVPRIQCEDCGDPQGLKDNSQFCQRIQROGLAFYKHLSDIFKGEPAALLPDS 120
QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQWQORPLLRSKILRSLOAFLAIAARV 180
DB 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQWQORPLLRSKILRSLOAFLAIAARV 180
QY 181 FAHGAATLTPELVPTA 196
DB 181 FAHGAATLTPELVPTA 196
RESULT 3
AAW01982
ID AAW01982 standard; Protein; 196 AA.
XX
XX AAW01982;
AC
XX
XX 27-SEP-2000 (first entry)
DT
XX
XX Murine interleukin-B30 (IL-B30).
DE
XX
XX Interleukin-B30; IL-B30; murine; mouse; cytokine; cellular signalling;
KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
KW granulocyte colony stimulating factor; immune disorder;

```

inflammatory disease; autoimmune disease; antigen; antibody.

Mus sp.

Key Location/Qualifiers  
 Peptide 1..21  
 Protein /note= "Signal peptide"  
 /note= "Mature murine IL-B30"

US06060284-A.

09-MAY-2000.

24-JUL-1998; 98US-0122443.

25-JUL-1997; 97US-0053765.

(SCHE ) SCHERING CORP.

Bazan JF;

WPI; 2000-364420/31.

N-PSDB; AAA52578.

Novel recombinant DNA encoding cytokines especially interleukin-B30 useful as probes or primers for diagnosing immune disorders including autoimmune or chronic inflammatory conditions -

Claim 1; Column 7-10; 32pp; English.

This sequence represents murine interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte colony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role of IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages. Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and antagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a source of probes and primers. The IL-B30 probes and primers can be used to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used to detect levels of IL-B30 protein in a sample.

Sequence 196 AA;

Query Match 100.0%; Score 1038; DB 21; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCRAVIMLWLPWYTOGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MLCRAVIMLWLPWYTOGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMNLLREE 60

QY 61 EDEETNNVPRIQCEGDCPDQGLKDNSQFCLOIRIQGLAFYKHLSDIFKGEPAALLPDS 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 EDEETNNVPRIQCEGDCPDQGLKDNSQFCLOIRIQGLAFYKHLSDIFKGEPAALLPDS 120

QY 121 PMEQLHTSLGLSQLLPEDHPRETQMPSLSSSQWQRPRLRSKILRSQAFLAIAARV 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 PMEQLHTSLGLSQLLPEDHPRETQMPSLSSSQWQRPRLRSKILRSQAFLAIAARV 180

QY 181 FAHGAATLTLEPLVPTA 196  
 ||||||||||||||||||  
 Db 181 FAHGAATLTLEPLVPTA 196

RESULT 4  
 AAB47121  
 ID AAB47121 standard; Protein; 196 AA.  
 XX  
 AC AAB47121;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE Murine IL-B30.  
 XX  
 KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
 KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;  
 KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
 KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
 KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
 KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
 KW Castleman's disease.  
 XX  
 OS Mus musculus.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /note= "Signal peptide"  
 FT /note= "Mature protein"  
 XX  
 PN WO200118051-A2.  
 XX  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-US24686.  
 XX  
 PR 09-SEP-1999; 99US-0393090.  
 PR 10-NOV-1999; 99US-0164616.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
 PI Wiekowski MT, Lira SA, Narula SK;  
 XX  
 DR WPI; 2001-244560/25.  
 DR N-PSDB; AAC85541.  
 XX  
 PT Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
 PT segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
 PT atherosclerosis, multiple sclerosis, vasculitis and tumour -  
 PS Disclosure; Page 11-12; 69pp; English.  
 XX  
 CC This sequence shows mouse interleukin-B30. Fragments of this protein  
 CC may be used in the composition of the invention. The composition  
 CC comprises a substantially pure polypeptide comprising a number of  
 CC distinct segments of at least 7 contiguous amino acids from IL-12 p40  
 CC and/or IL-B30, and a substantially pure polypeptide comprising a  
 CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
 CC IL-B30. The composition is useful for modulating physiology or  
 CC development of a cell or tissue in a host organism, resulting in an  
 CC increased or decreased production of Interferon-gamma (IFNgamma), an  
 CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
 CC anti-viral effect or antagonized allergic effect, and amelioration  
 CC of an autoimmune condition or a chronic inflammatory condition  
 CC IL-B30 or its agonist is useful inducing the proliferation of memory  
 CC T-cells. An agonist or antagonist of IL-B30 protein is useful for  
 CC modulating the trafficking or activation of a leukocyte in an animal  
 CC experiencing science or symptoms of autoimmunity, an inflammatory  
 CC condition, tissue specific autoimmunity, degenerative autoimmunity,  
 CC rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
 CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
 CC transplant, spinal injury, stroke, neurodegeneration, an infectious  
 CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
 CC disease, postmenopausal osteoporosis or IL-6-associated diseases.

```
CC IL-12 p40/IL-B30 is useful as an immunogen for the production a
CC antisera or antibodies specific for binding.
XX
SQ Sequence 196 AA;
Query Match 100.0%; Score 1038; DB 22; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.2e-99;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60
Db 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60
Qy 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCQLRIROGLAFYKHLSDIFKGPALLPDS 120
Db 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCQLRIROGLAFYKHLSDIFKGPALLPDS 120
Qy 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSLSQQWQRPRLRSKILRSIQAFIAIARV 180
Db 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSLSQQWQRPRLRSKILRSIQAFIAIARV 180
Qy 181 FAHGAATLTPELVPTA 196
Db 181 FAHGAATLTPELVPTA 196
RESULT 5
AAAY29783
ID AAY29783 standard; Protein; 189 AA.
AC AAY29783;
XX
DT 04-NOV-1999 (first entry)
DE Human interleukin B30.
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
KW interleukin B30; DCRS1; IL-B30; cytokine receptor; diagnosis;
KW inflammatory disorder; inflammatory response; innate immunity;
KW morphogenic development; immunological disorder.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= signal
FT 22..189
FT /label= IL-B30
XX
PN WO9940195-A1.
XX
PD 12-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US02600.
XX
PR 13-MAY-1998; 98US-0078194.
PR 06-FEB-1998; 98US-0073941.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Kastelein RA, Mattson JD, McClanahan TK;
XX
XX WPI; 1999-527306/44.
XX
XX N-PSDB; AAZ08865.
XX
XX New receptor subunits useful in the treatment inflammatory disorders
XX
XX Claim 2; Page 26-27; 133pp; English.
XX
XX The 'present invention describes a composition (I) comprising DNAX
XX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
XX subunit I (DCRS1) protein, which together encode a new mammalian
XX cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
CC
```

```
CC proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1
CC is useful for screening for ligands (i.e. agonists/antagonists) from
CC a library of compounds, which are useful for modulating the physiology
CC or development of a cell or tissue culture e.g. inflammatory responses,
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal expression of
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC and the subunits DCRS1 and DCRS1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the specifically claimed human IL-B30, for use in the
XX composition of the present invention.
XX
SQ Sequence 189 AA;
Query Match 69.2%; Score 718.5; DB 20; Length 189;
Best Local Similarity 74.6%; Pred. No. 1.8e-66;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps
Qy 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60
Db 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 59
Qy 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCQLRIROGLAFYKHLSDIFKGPALLPDS 120
Db 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCQLRIROGLAFYKHLSDIFKGPALLPDS 119
Qy 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSLSQQWQRPRLRSKILRSIQAFIAIARV 180
Db 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSLSQQWQRPRLRSKILRSIQAFIAIARV 179
Qy 181 FAHGAATLT 189
Db 181 FAHGAATLT 188
RESULT 6
AAW95002
ID AAW95002 standard; Protein; 189 AA.
XX
AC AAW95002;
XX
DT 21-MAY-1999 (first entry)
DE Human interleukin-B30 (IL-B30) polypeptide.
XX
KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferatio
KW inflammatory condition; drug screening; human.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT 22..189
FT /note= "mature protein"
XX
XX WO9905280-A1.
XX
XX 04-FEB-1999.
XX
XX 24-JUL-1998; 98WO-US15423.
XX
XX 25-JUL-1997; 97US-0900905.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Bazan JF;
XX
XX WPI; 1999-142935/12.
XX
XX N-PSDB; AAX17786.
XX
```

XX Newly isolated or recombinant polynucleotide encoding mammalian  
 PT cytokine interleukin-B30 (IL-B30), including fragments - useful for  
 PT regulating activation, development, differentiation and function of  
 PT various cell types, and for diagnosing and treating conditions  
 PT associated with IL-B30  
 XX  
 PS Claim 2; Page 8-9; 83pp; English.  
 PS  
 CC This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.  
 CC Host cells containing a vector comprising the IL-B30 nucleic acid are  
 CC used for the recombinant production of the protein. The polynucleotides  
 CC are useful for diagnosis of IL-B30 mediated conditions, and forensic  
 CC science (e.g. to distinguish rodent from human, or as a marker to  
 CC distinguish between different cells exhibiting differential expression or  
 CC modification patterns). The IL-B30 (including fragments), together with  
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They  
 CC are also used for treating conditions associated with abnormal physiology  
 CC or development, including inflammatory conditions. The polypeptide  
 CC cytokine should mediate cytokine synthesis and proliferation in cells.  
 CC IL-B30 is useful for drug screening to identify compounds having binding  
 CC affinity to IL-B30.  
 XX  
 SQ Sequence 189 AA;

Query Match 69.2%; Score 718.5; DB 20; Length 189;  
 Best Local Similarity 74.6%; Pred. No. 1.8e-66;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLDCAVIMLWLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60  
 DB 1 MLGSRVIMLWLLPMTAQGRAVPGGSPAWTQCQQLSKLCTLAWSAHLVGHMD-LREE 59  
 QY 61 EDEETKNVPRIOCGDQGLKDNQFCQIRQGLAFYKHLSDIFKGEPAALLPDS 120  
 DB 60 GDEETNDVPHIQCGDQGLKDNQFCQIRQGLAFYKHLSDIFKGEPAALLPDS 119  
 QY 121 PMEQLHTSLGLSQLQPEDHPRETQMPSSSQWQRPRLRSKILRSQAFLAIAARV 180  
 DB 120 PVAQLHASLLGLSQLQPEGHWHETQIIPSLSPSQWQRLRLRSKILRSQAFLAIAARV 179  
 QY 181 FAHGAATLT 189  
 DB 180 FAHGAATLS 188

RESULT 7  
 AAB01981  
 ID AAB01981 standard; Protein; 189 AA.  
 AC AAB01981;  
 XX  
 XX 27-SEP-2000 (first entry)  
 DT Human interleukin-B30 (IL-B30).  
 DE Interleukin-B30; IL-B30; human; cytokine; cellular signalling;  
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
 KW granulocyte colony stimulating factor; immune disorder;  
 KW inflammatory disease; autoimmune disease; antigen; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..21  
 FT Peptide /note= "Signal peptide"  
 FT Protein 22..189  
 FT /note= "Mature human IL-B30"  
 XX  
 PN US6060284-A.  
 XX  
 XX 09-MAY-2000.  
 PD  
 XX

PF 24-JUL-1998; 98US-0122443.  
 XX  
 PR 25-JUL-1997; 97US-0053765.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Bazan JF;  
 XX  
 XX WPI; 2000-364420/31.  
 DR N-PSDB; AAA52577.  
 DR  
 XX Novel recombinant DNA encoding cytokines especially interleukin-B30  
 PT useful as probes or primers for diagnosing immune disorders including  
 PT autoimmune or chronic inflammatory conditions  
 PT  
 XX Claim 1; Column 5-8; 32pp; English.  
 PS  
 CC This sequence represents human interleukin-B30 (IL-B30). IL-B30  
 CC is a novel cytokine, exhibiting significant homology to IL-6 and  
 CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical  
 CC role in signalling between immune or other cells during an immune  
 CC response. The precise role of IL-B30 is not yet known - it is likely  
 CC to have either a stimulatory or an inhibitory effect on haematopoietic cells  
 CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.  
 CC Alternatively, it may affect vascular physiology or development, or have  
 CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and  
 CC antagonists are useful in the diagnosis and treatment of disorders  
 CC associated with abnormal expression or activity of IL-B30 e.g.,  
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are  
 CC useful for recombinant expression of IL-B30 in a host cell, and as a  
 CC source of probes and primers. The IL-B30 probes and primers can be used  
 CC to detect levels of IL-B30 expression in samples from patients suspected  
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may  
 CC also be used to identify homologous genes in other species. IL-B30  
 CC protein or its fragments are useful as antigens for raising antibodies to  
 CC various linear and conformational epitopes. Such antibodies may be used  
 CC to detect levels of IL-B30 protein in a sample.  
 XX  
 SQ Sequence 189 AA;

Query Match 69.2%; Score 718.5; DB 21; Length 189;  
 Best Local Similarity 74.6%; Pred. No. 1.8e-66;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLDCAVIMLWLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60  
 DB 1 MLGSRVIMLWLLPMTAQGRAVPGGSPAWTQCQQLSKLCTLAWSAHLVGHMD-LREE 59  
 QY 61 EDEETKNVPRIOCGDQGLKDNQFCQIRQGLAFYKHLSDIFKGEPAALLPDS 120  
 DB 60 GDEETNDVPHIQCGDQGLKDNQFCQIRQGLAFYKHLSDIFKGEPAALLPDS 119  
 QY 121 PMEQLHTSLGLSQLQPEDHPRETQMPSSSQWQRPRLRSKILRSQAFLAIAARV 180  
 DB 120 PVAQLHASLLGLSQLQPEGHWHETQIIPSLSPSQWQRLRLRSKILRSQAFLAIAARV 179  
 QY 181 FAHGAATLT 189  
 DB 180 FAHGAATLS 188

RESULT 8  
 AAB47120  
 ID AAB47120 standard; Protein; 189 AA.  
 XX  
 AC AAB47120;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE Human IL-B30.  
 XX  
 KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
 KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;

KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
KW Castleman's disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..189  
FT /note= "Mature protein"  
XX  
XX W0200118051-A2.  
XX  
XX 15-MAR-2001.  
XX  
XX 08-SEP-2000; 2000WO-US24686.  
XX  
XX 09-SEP-1999; 99US-0393090.  
XX 10-NOV-1999; 99US-0164616.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Opmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
PI Wiekowski MT, Lira SA, Narula SK;  
XX  
XX WPI; 2001-244560/25.  
XX N-PSDB; AAC85540.  
XX  
XX Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
XX segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
XX atherosclerosis, multiple sclerosis, vasculitis and tumour  
XX  
XX Disclosure; Page 10-11; 69pp; English.  
XX  
XX This sequence shows human interleukin-B30. Fragments of this protein  
XX may be used in the composition of the invention. The composition  
XX comprises a substantially pure polypeptide comprising a number of  
XX distinct segments of at least 7 contiguous amino acids from IL-12 p40  
XX and/or IL-B30, and a substantially pure polypeptide comprising a  
XX segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
XX IL-B30. The composition is useful for modulating physiology or  
XX development of a cell or tissue in a host organism, resulting in an  
XX increased or decreased production of Interferon-gamma (IFNgamma), an  
XX enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
XX anti-viral effect or antagonized allergic effect, and amelioration  
XX of an autoimmune condition or a chronic inflammatory condition.  
XX IL-B30 or its agonist is useful inducing the proliferation of memory  
XX T-cells. An agonist or antagonist of IL-B30 protein is useful for  
XX modulating the trafficking or activation of a leukocyte in an animal  
XX experiencing science or symptoms of autoimmunity, an inflammatory  
XX condition, tissue specific autoimmunity, degenerative autoimmunity,  
XX rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
XX sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
XX transplant, spinal injury, stroke, neurodegeneration, an infectious  
XX disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
XX disease, postmenopausal osteoporosis or IL-6-associated diseases.  
XX IL-12 p40/IL-B30 is useful as an immunogen for the production a  
XX antiserum or antibodies specific for binding.  
XX  
SQ Sequence 189 AA;  
  
Query Match 69.2%; Score 718.5; DB 22; Length 189;  
Best Local Similarity 74.6%; Pred. No. 1 8e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
  
QY 1 MLDCAVIMLMLPVWVTOGLAVPRSSPDWAQCOOLGRNLCMLAWNAHAPAGHNNLLREE 60  
DB 1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHLPLVGHMD-LREE 59  
QY 61 EDEETKNVPRVQCEGDCDPOGLRDNQSFCLQRTHOGLIFVEKILGSDIFTGPESLLPDS 120

Db . 60 GDEETNDVPHIQCGDCDPOGLRDNQSFCLQRTHOGLIFVEKILGSDIFTGPESLLPDS 119  
QY 121 PMEQLHYSLLGLSOLLQPEDHPRETQQMPSLSSQQWQRLLRSKILRSLOAFATAARV 180  
DB 120 PVAQLHASLLGLSOLLQPEGHWHETQQTIPSLSPSQWQRLLRFRKILRSLOAFVAARV 179  
QY 181 FAHGAATLT 189  
DB 180 FAHGAATLS 188  
  
RESULT 9  
AA94966  
ID AA94966 standard; Protein; 189 AA.  
XX  
XX AA94966;  
XX  
XX 16-JUN-2000 (first entry)  
XX Human secreted protein clone rk80\_3 protein sequence SEQ ID NO:138.  
KW Human; secreted protein; immunostimulant; immunosuppressant; virucide;  
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;  
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;  
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;  
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;  
KW connective tissue disease; multiple sclerosis; erythematosis;  
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;  
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;  
KW insulin dependent diabetes mellitus; graft-versus-host-disease;  
KW autoimmune inflammatory eye disease; allergy.  
OS Homo sapiens.  
XX  
XX W0200009552-A1.  
XX  
XX 24-FEB-2000.  
XX  
XX 13-AUG-1999; 99WO-US18298.  
XX  
XX 14-AUG-1998; 98US-0096622.  
XX 17-AUG-1998; 98US-0096815.  
XX 04-SEP-1998; 98US-0099229.  
XX 23-OCT-1998; 98US-0105368.  
XX 08-JAN-1999; 99US-0115234.  
XX 12-FEB-1999; 99US-0119931.  
XX 18-FEB-1999; 99US-0120575.  
XX 30-APR-1999; 99US-0132020.  
XX 11-AUG-1999; 99US-0096622.  
XX (GEMY ) GENETICS INST INC.  
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
PI Wong GG, Clark HF, Fechtel K;  
XX  
XX WPI; 2000-205979/18.  
XX  
XX New polynucleotides encoding secreted proteins, which may have e.g.  
XX nutritional, chemokine, immune stimulating or suppressing,  
XX hematopoiesis regulating, tissue growth, activin/inhibin  
XX antiinflammatory or tumor inhibition activity  
XX  
PS Claim 147; Page 597; 641pp; English.  
XX  
XX AAA16618 to AAA16697 encode the human secreted proteins given in  
XX AA94988 to AA94980 isolated from human adult brain, adult thyroid,  
XX adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,  
XX adult placenta, adult testis, whole embryo, adult cartilage, kidney,  
XX foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,  
XX and adult bladder, cDNA libraries. The polynucleotides and proteins are  
XX predicted to have biological activities which would make them suitable

CC for treating, preventing or ameliorating medical conditions in humans  
CC and animals. The polynucleotides can be used as markers for tissues in  
CC which the protein is preferentially expressed, as molecular weight  
CC markers on Southern gels, and as chromosome markers or tags to identify  
CC chromosomes or to map gene positions. The proteins can be used in the  
CC treatment of immune deficiencies and disorders, such as severe combined  
CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
CC infections. These infections include human immunodeficiency virus (HIV),  
CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
CC candidiasis. The proteins can be used to treat autoimmune disorders such  
CC as connective tissue disease, multiple sclerosis, systemic lupus  
CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,  
CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and  
CC autoimmune inflammatory eye disease. The proteins can also be used to  
CC treat allergic conditions, such as asthma. AA16698 to AA16774 represent  
CC probes for the human secreted proteins from the present invention.  
XX  
SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLLPWTQGLAVPRSSPDWAOQQLSRNLCMLAWNAHAPAGHMLNLR 60  
DB 1 MLGSRVAMLLLLPWTAGRAVPGGSPAWTQCQLSKLCTLAWSAFLVGHMD-LREE 59  
QY 61 EDEETKNVPRIQCEDGCDPQGLKNSQFCIQRIQGLAFYKHLLDSDFKGEPAALPDS 120  
DB 60 GDEETNDVPHIQCGDGDPOGLRDNQFCIQRIHQGLIFYEKLGLSDIFTGEPSSLPDS 119  
QY 121 PMEQLHTSLGLSLLQLOPEDHPRETQOMPSSSSQOWORPLLRSLKILRSLOAFIAIARV 180  
DB 120 PVQQLHASLLGLSLLQLOPEGHWHETQOIPSLSPSQWQRLRLRFLKILRSLOAFVAVARV 179  
QY 181 FAHGAATLT 189  
DB 180 FAHGAATLS 188

## RESULT 10

ID AAY54606 standard; Protein; 189 AA.  
XX  
AC AAY54606;  
XX  
DT 01-FEB-2000 (first entry)  
XX  
DE SGRF protein sequence.  
XX  
KW SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;  
KW immune system; haematopoietic system; therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO954357-A1.  
XX  
PD 28-OCT-1999.  
XX  
PF 14-APR-1999; 99WO-JP01997.  
XX  
PR 14-APR-1998; 98JP-0121805.  
XX  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
PI Hirata Y;  
XX  
DR WPI: 2000-013230/01.  
DR N-PSDB; AA237262, AA237263.  
XX  
PT Novel cytokine-like protein, with activity of supporting proliferation  
of myeloid cells, useful in treating abnormality of cell proliferation

PT In immune and haematopoiesis systems -  
XX  
PS Claim 1: Fig 1; 69pp; Japanese.  
XX  
CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)  
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF  
CC family. The protein can be used in drugs for treating diseases due to  
CC abnormality of cell proliferation in the immune system and haematopoietic  
CC system.  
XX  
SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLLPWTQGLAVPRSSPDWAOQQLSRNLCMLAWNAHAPAGHMLNLR 60  
DB 1 MLGSRVAMLLLLPWTAGRAVPGGSPAWTQCQLSKLCTLAWSAFLVGHMD-LREE 59  
QY 61 EDEETKNVPRIQCEDGCDPQGLKNSQFCIQRIQGLAFYKHLLDSDFKGEPAALPDS 120  
DB 60 GDEETNDVPHIQCGDGDPOGLRDNQFCIQRIHQGLIFYEKLGLSDIFTGEPSSLPDS 119  
QY 121 PMEQLHTSLGLSLLQLOPEDHPRETQOMPSSSSQOWORPLLRSLKILRSLOAFIAIARV 180  
DB 120 PVQQLHASLLGLSLLQLOPEGHWHETQOIPSLSPSQWQRLRLRFLKILRSLOAFVAVARV 179  
QY 181 FAHGAATLT 189  
DB 180 FAHGAATLS 188

## RESULT 11

AAU12287  
ID AAU12287 standard; Protein; 189 AA.  
XX  
AC AAU12287;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human PRO5798 polypeptide sequence.  
XX  
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
KW adipocyte; A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO200140466-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 01-DEC-2000; 2000WO-US32678.  
XX  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 08-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31243.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.



XX SQ Sequence 189 AA;  
Query Match 69.1%; Score 717.5; DB 22; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLDCAVIMLLPWVTQGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60  
II III:II III III III III:II III:II III:II III:II  
DB 1 MGSRAVMLLLPWTAGRAVPGSSPAWTQCQQLSQKLTCTLAWSAHPVLVGHMD-LREE 59  
QY 61 EDEETKNNVPRIQEDGCDPGGLKNDNSQFCLQRTQGLAYKHLSDSDIFKGPALLPDS 120  
III:II III III III:II III:II III:II III:II III:II III:II  
DB 60 GDEETNDVPHIQCGDGPQGLRNSQFCLQRTQGLAYKHLSDSDIFKGPALLPDS 119  
QY 121 PNEQLHTSLGLSQLQDPEDHPRETQOMPSLSSSQWQRPRLRSKILRSLOAFIATAARV 180  
II III:II III III III III:II III III III III:II III:II III:II  
DB 120 PVGQLHASLGLSQLQDPEDHPRETQOMPSLSSSQWQRPRLRSKILRSLOAFIATAARV 179  
QY 181 FAHGAATLT 189  
II III:II III III III III:II III III III III:II III:II III:II  
DB 180 FAHGAATLS 188  
RESULT 13  
AAY29787  
ID AAY29787 standard; Protein; 102 AA.  
XX AC AAY29787;  
XX DE Partial pig interleukin B30 protein.  
XX KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW interleukin B30; DSRs1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX OS Sus scrofa.  
XX PN WO9940195-A1.  
XX PD 12-AUG-1999.  
XX PF 05-FEB-1999; 99WO-US02600.  
XX PR 13-MAY-1998; 98US-0078194.  
XX PR 06-FEB-1998; 98US-0073941.  
XX PA (SCHE ) SCHERING CORP.  
XX PI Kastelein RA, Mattson JD, McClanahan TK;  
XX WPI; 1999-527306/44.  
XX PT New receptor subunits useful in the treatment inflammatory disorders  
XX PS Disclosure; Page 29; 133pp; English.  
XX CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor  
CC subunit 1 (DSRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSRs1 and DCRS1 are useful as immunogens for generating

CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the partial pig IL-B30, given in the present invention.  
XX SQ Sequence 102 AA;  
Query Match 34.3%; Score 356; DB 20; Length 102;  
Best Local Similarity 72.3%; Pred. No. 3.8e-29;  
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;  
QY 90 CLQRTQGLAYKHLSDSDIFKGPALLPSPMEQLHTSLGLSQLQDPEDHPRETQOMP 149  
II III:II III III III III:II III:II III:II III:II III:II  
DB 2 CLQRTQGLAYKHLSDSDIFKGPALLPSPMEQLHTSLGLSQLQDPEDHPRETQOMP 61  
QY 150 SILSSSQWQRPRLRSKILRSLOAFIATAARVFAHGAATLT 190  
II III:II III III III III:II III III III III:II III:II III:II  
DB 62 SFSPSQWQRPRLRSKILRSLOAFIATAARVFAHGAATLT 102  
RESULT 14  
AAW95004  
ID AAW95004 standard; peptide; 102 AA.  
XX AC AAW95004;  
XX DT 21-MAY-1999 (first entry)  
XX DE Pig interleukin-B30 (IL-B30) polypeptide.  
XX KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
KW inflammatory condition; drug screening; pig.  
XX OS Sus scrofa.  
XX PN WO9905280-A1.  
XX PD 04-FEB-1999.  
XX PF 24-JUL-1998; 98WO-US15423.  
XX PR 25-JUL-1997; 97US-0900905.  
XX PA (SCHE ) SCHERING CORP.  
XX PI Bazan JF;  
XX WPI; 1999-142935/12.  
XX PT Newly isolated or recombinant polynucleotide encoding mammalian  
PT cytokine interleukin-B30 (IL-B30), including fragments useful for  
PT regulating activation, development, differentiation and function of  
PT various cell types, and for diagnosing and treating conditions  
PT associated with IL-B30  
XX PS Claim 1; Page 11-12; 83pp; English.  
XX CC This invention relates to mammalian cytokine interleukin-B30 (IL-B30)  
CC polypeptides. Host cells containing a vector comprising the IL-B30  
CC nucleic acids are used for the recombinant production of the proteins.  
CC The polynucleotides are useful for diagnosis of IL-B30 mediated  
CC conditions, and forensic science (e.g. to distinguish rodent from human,  
CC or as a marker to distinguish between different cells exhibiting  
CC differential expression or modification patterns). The IL-B30 (including  
CC fragments), together with antibodies that bind to IL-B30 are useful for  
CC teaching purposes. They are also used for treating conditions associated  
CC with abnormal physiology or development, including inflammatory  
CC conditions. The polypeptide cytokine should mediate cytokine synthesis  
CC and proliferation in cells. IL-B30 is useful for drug screening to  
CC identify compounds having binding affinity to IL-B30. The present  
XX sequence represents a pig IL-B30.  
XX SQ Sequence 102 AA;



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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:54:30 : Search time 7.63636 Seconds  
(without alignments)  
401.978 Million cell updates/sec

Title: US-09-658-699-4

Perfect score: 1038

Sequence: 1 MLCRAVIMLLPWTQGL.....AARFAHGAATLPIVPTA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	88	8.5	181	10	US-09-764-864-1144
2	88	8.5	181	10	US-09-764-864-1144
3	84	8.1	212	10	US-09-854-280-14
4	84	8.1	212	10	US-09-854-280-14
5	81.5	7.9	175	10	US-09-754-532-71
6	79.5	7.7	175	10	US-09-754-532-72
7	78.5	7.6	175	10	US-09-754-532-73
8	78.5	7.6	175	10	US-09-754-532-74
9	78.5	7.6	175	10	US-09-754-532-75
10	78	7.5	285	10	US-09-754-532-76
11	77.5	7.5	348	12	US-10-003-496-1
12	76.5	7.4	174	10	US-09-760-008A-1
13	76.5	7.4	174	10	US-09-950-473-2
14	76.5	7.4	174	12	US-10-016-403-1
15	76.5	7.4	174	12	US-10-016-403-2
16	76.5	7.4	174	12	US-10-016-403-3
17	76.5	7.4	174	12	US-10-003-496-1
18	76.5	7.4	175	10	US-09-754-532-2
19	76.5	7.4	175	10	US-09-754-532-67

20	76.5	7.4	175	10	US-09-754-532-68	Sequence 68, Appl
21	76.5	7.4	175	10	US-09-754-532-69	Sequence 69, Appl
22	76.5	7.4	175	10	US-09-754-532-70	Sequence 70, Appl
23	76.5	7.4	175	10	US-09-754-532-71	Sequence 71, Appl
24	76.5	7.4	175	10	US-09-754-532-72	Sequence 72, Appl
25	76.5	7.4	175	10	US-09-754-532-73	Sequence 73, Appl
26	76.5	7.4	175	10	US-09-754-532-74	Sequence 74, Appl
27	76.5	7.4	175	10	US-09-754-532-75	Sequence 75, Appl
28	76.5	7.4	175	10	US-09-754-532-76	Sequence 76, Appl
29	76.5	7.4	175	10	US-09-754-532-77	Sequence 77, Appl
30	76.5	7.4	175	10	US-09-754-532-78	Sequence 78, Appl
31	76.5	7.4	175	10	US-09-754-532-83	Sequence 83, Appl
32	76.5	7.4	175	10	US-09-754-532-84	Sequence 84, Appl
33	76.5	7.4	175	10	US-09-754-532-85	Sequence 85, Appl
34	76.5	7.4	175	10	US-09-754-532-86	Sequence 86, Appl
35	76.5	7.4	175	10	US-09-754-532-87	Sequence 87, Appl
36	76.5	7.4	175	10	US-09-754-532-88	Sequence 88, Appl
37	76.5	7.4	175	10	US-09-754-532-89	Sequence 89, Appl
38	76.5	7.4	175	10	US-09-754-532-94	Sequence 94, Appl
39	76.5	7.4	175	10	US-09-754-532-95	Sequence 95, Appl
40	76.5	7.4	175	10	US-09-754-532-96	Sequence 96, Appl
41	76.5	7.4	175	10	US-09-754-532-97	Sequence 97, Appl
42	76.5	7.4	175	10	US-09-754-532-99	Sequence 99, Appl
43	76.5	7.4	175	10	US-09-754-532-100	Sequence 100, App
44	76.5	7.4	175	10	US-09-754-532-101	Sequence 101, App
45	76.5	7.4	175	10	US-09-754-532-102	Sequence 102, App

ALIGNMENTS

RESULT 1  
US-09-764-864-1144  
; Sequence 1144, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764.864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1144  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-764-864-1144

Query Match 8.5%; Score 88; DB 10; Length 181;  
Best Local Similarity 23.7%; Pred. No. 0.057;  
Matches 47; Conservative 19; Mismatches 50; Indels 82; Gaps 11;

Qy	11	WLLPWVTOGLAVPRSSP-----DWAQCQOLSRNLCMLAWNAHA-PAGHMNLLREEDEET	65
Db	8	WLLPKPSGICLPGTWAPPGSSHWVACGL-----WGPGAGPA-----	45
Qy	66	KNVPRIQEDGCDPOGLKDNSQFCLOIRIQL-----AFYKHLIDS-DIF	110
Db	46	-----TGSQPWGKE-----RRARLGCFFPHSPWTLREELSWAGCHVSDSGDVM	89
Qy	111	KGEAL-----LPDPSMEQLHTSLGLSQLLOPDHPRETQOMPSLSSSQWQRP-----	160
Db	90	GGHRSVAGYWEFFLSFLSSLHPFSGMCL-----PR--SRSPSPSPQWKKPVIDTA	139
Qy	161	-----LLRSKILRSLOAFL	174
Db	140	VGGRCKSLTFGALEGL	157

RESULT 2  
US-09-764-864-1559



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; *COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-80
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Query Match 7.9%; Score 81.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.26;
Matches 35; Conservative 17; Mismatches 36; Indels 27; Gaps 7;

QY 90 CLQRIROGLAFYKHLSDIFKG-EPALLPDSMPQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLFLYQGLQA--LEGISPELGPTLDTQLDQVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ-QMPSSSQWQRPRLRSKILRSLOAFIAIAARVFAHGAATLTPE 191
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLAH----LAQP 175
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RESULT 6
US-09-754-532-79
; Sequence 79, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
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;
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-79
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Query Match 7.7%; Score 79.5; DB 10; Length 175;
Best Local Similarity 30.9%; Pred. No. 0.42;
Matches 34; Conservative 16; Mismatches 37; Indels 23; Gaps 6;

QY 90 CLQRIROGLAFYKHLSDIFKG-EPALLPDSMPQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLFLYQGLQA--LEGISPELGPTLDTQLDQVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ-QMPSSSQWQRPRLRSKILRSLOAFIAIAARVFAHGAATLTPE 186
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLRLAA 174
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RESULT 7
US-09-754-532-92
; Sequence 92, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-92
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Query Match 7.6%; Score 78.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.54;
Matches 35; Conservative 16; Mismatches 37; Indels 27; Gaps 7;

QY 90 CLQRIROGLAFYKHLSDIFKG-EPALLPDSMPQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLFLYQGLQA--LEGISPELGPTLDTQLDQVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ-QMPSSSQWQRPRLRSKILRSLOAFIAIAARVFAHGAATLTPE 191
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLRH----LAQP 175

RESULT 8
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```

Query Match          7.6%; Score 78.5; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

QY  90 CLCIRQIGLAIFYKHLILSDIFKQ-EPALLPDSPEMEQLHTSL-----LGLSLQLIQ 137
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB  75 CLSQLSHGLFYQGLLQA--LEGISPELGPPTLDTQLDVAFAATTIQQWEEIGMAPALQ 132

QY  138 PEDHPRETQ-QMPSLSSSQWQRPLLRSLKILRSLOAFALATAARVFAHGAATITEP 191
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB  133 P-----TOGAMPAPASA--FORRAGGVLVASHLQSFLEYSYKVLRH----LAQP 175

RESULT 9
US-09-754-532-109
; Sequence 109, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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ORGANISM: *Pseudomonas aeruginosa*  
US-09-815-242-5068





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 11:53:05 ; Search time 12.2182 Seconds  
(without alignments)  
471.993 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLDICRAVIMLWLLPWVTOGL.....AARVFAHGAATLPELVPVTA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_A1.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	100.0	196	3	US-09-122-443-4
2	718.5	69.2	189	3	US-09-122-443-2
3	356	34.3	102	3	US-09-122-443-5
4	112	10.8	162	4	US-09-499-148-5
5	112	10.8	184	3	US-09-122-443-13
6	104	10.0	162	4	US-09-499-148-2
7	103	9.9	166	4	US-09-499-148-3
8	100	9.6	166	4	US-09-499-148-9
9	96	9.2	166	4	US-09-499-148-7
10	96	9.2	188	3	US-09-122-443-14
11	96	9.2	211	4	US-08-097-869-8
12	92.5	8.9	186	1	US-08-209-182C-6
13	92.5	8.9	186	5	PCT-US92-05612-6
14	91	8.8	166	4	US-09-499-148-6
15	89	8.6	212	4	US-09-487-792-14
16	88	8.5	184	2	US-08-693-182-2
17	88	8.5	184	2	US-09-008-482-2
18	88	8.5	185	1	US-07-918-181A-4
19	88	8.5	185	1	US-08-231-575-4
20	88	8.5	165	5	PCT-US93-06928-4
21	87.5	8.4	152	2	US-08-716-317-10
22	87.5	8.4	163	2	US-08-716-317-15
23	86.5	8.3	174	3	US-09-122-443-7
24	86.5	8.3	319	5	PCT-US94-04208-2
25	86.5	8.3	337	3	US-08-469-318-148
26	86.5	8.3	337	3	US-08-468-609A-148
27	86.5	8.3	337	4	US-08-446-872A-148

28	86.5	8.3	337	4	US-08-762-227A-148	Sequence 148, App
29	86.5	8.3	337	5	PCT-US95-01185-148	Sequence 148, App
30	86	8.3	185	1	US-07-918-181A-8	Sequence 8, Appl
31	86	8.3	185	1	US-08-231-575-8	Sequence 8, Appl
32	86	8.3	185	5	PCT-US93-06928-8	Sequence 8, Appl
33	84.5	8.1	185	5	PCT-US92-05612-2	Sequence 2, Appl
34	84.5	8.1	186	1	US-08-209-182C-2	Sequence 2, Appl
35	84	8.1	164	4	US-08-318-193-60	Sequence 60, Appl
36	84	8.1	166	4	US-09-499-148-1	Sequence 1, Appl
37	84	8.1	183	1	US-08-009-973-1	Sequence 1, Appl
38	84	8.1	184	1	US-08-567-047-2	Sequence 2, Appl
39	84	8.1	184	2	US-08-567-048-2	Sequence 2, Appl
40	84	8.1	184	6	5186931-1	Patent No. 5186931
41	84	8.1	185	1	US-07-632-070B-1	Sequence 1, Appl
42	84	8.1	185	1	US-07-918-181A-2	Sequence 2, Appl
43	84	8.1	185	1	US-08-231-575-2	Sequence 2, Appl
44	84	8.1	185	1	US-08-246-427A-5	Sequence 5, Appl
45	84	8.1	185	2	US-08-716-317-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-122-443-4  
; Sequence 4, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-122-443-4

Query Match 100.0%; Score 1038; DB 3; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.le-109;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLDICRAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60  
DB 1 MLDICRAVIMLWLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREE 60

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QY 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCLOQRIQGLAFYKHLSDIFKGEPAALLPDS 120
|||||
DB 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCLOQRIQGLAFYKHLSDIFKGEPAALLPDS 120
|||||
QY 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWORPLRSKILRSLOAFLAIAARV 180
|||||
DB 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWORPLRSKILRSLOAFLAIAARV 180
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QY 181 FAHGAATLTPELVPTA 196
|||||
DB 181 FAHGAATLTPELVPTA 196
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RESULT 2
US-09-122-443-2
; Sequence 2, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-122-443-2

Query Match 69.2%; Score 718.5; DB 3; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.5e-73;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLWLLPWVTGGLAVPRSSPDWAQCOOLRNLCMLAWNAPAGHMNLLREE 60
|||||
DB 1 MLGSRVIMLWLLPWVTAGRAVPGSGSPAWTQCQOLSKJCTLWASAPLVGHMD-LREE 59
|||||
QY 61 EDEETKNNVPRIQCEGCDPQGLKDNSQFCLOQRIQGLAFYKHLSDIFKGEPAALLPDS 120
|||||
DB 60 GDEETNDVPHIQCGDGPQGLRDNDSQFCLOQRIHQGLIFVEKLGSDIFTGEPSSLPDS 119
|||||
QY 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWORPLRSKILRSLOAFLAIAARV 180
|||||
DB 120 PVAQLHASLLGSLQLLPQEPGHWHWETQOIPSLSPSQPWQRLRLRKILRSLOAFVAARV 179
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QY 181 FAHGAATLT 189
|||||
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DB 180 FAHGAATLS 188
|||||

RESULT 3
US-09-122-443-5
; Sequence 5, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-5

Query Match 34.3%; Score 356; DB 3; Length 102;
Best Local Similarity 72.3%; Pred. No. 9.1e-33;
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps

QY 90 CLQRIQGLAFYKHLSDIFKGEPAALLPDS PMEOLHTSLGLSOLLQPEDHPRETQOMP 149
|||||
DB 2 CLQRIHQGLVFEYKELGSDIFTGEPSPDGSVQGLHASLLGRLQLLPQEGHHWETQTP 61
|||||
QY 150 SLSSSQOWORPLRSKILRSLOAFLAIAARVFAHGAATLT 190
|||||
DB 62 SPSPSQPWQRLRLRKILRSLOAFVAARVFAHGAATLSQ 102
|||||

RESULT 4
US-09-499-148-5
; Sequence 5, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIAANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
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; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-499-148-5

Query Match
Best Local Similarity 10.8%; Score 112; DB 4; Length 162;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNOSQFCQIRIQGLAFYKHLLD--S 107
Db 27 EKNDCEKSKETLAENKLLPKMEEKDGCQSGF--NQAICLIKTAGLLEYQIYLDLQ 84
QY 108 DIFKGEALLPDSPEQLHTSLGLSOLLO-----PEDHPRETQOMPSSLSQQWQ 158
Db 85 NEFEGN-----QETVMELQSSIRTLQILKEKIAGLITTPATH---TDMLEKMQSSNEW 136
QY 159 RPLRSKILRSLOAFIAAR 179
Db 137 KNAKVIIILRSLENFLOFSLR 157

RESULT 5
US-09-122-443-13
; Sequence 13, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bagan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Egwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-13

Query Match
10.8%; Score 112; DB 3; Length 184;
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Best Local Similarity 27.7%; Pred. No. 7.9e-05;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNOSQFCQIRIQGLAFYKHLLD--S 107
Db 49 EKNDCEKSKETLAENKLLPKMEEKDGCQSGF--NQAICLIKTAGLLEYQIYLDLQ 106
QY 108 DIFKGEALLPDSPEQLHTSLGLSOLLO-----PEDHPRETQOMPSSLSQQWQ 158
Db 107 NEFEGN-----QETVMELQSSIRTLQILKEKIAGLITTPATH---TDMLEKMQSSNEW 158
QY 159 RPLRSKILRSLOAFIAAR 179
Db 159 KNAKVIIILRSLENFLOFSLR 179
```

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RESULT 6
US-09-499-148-2
; Sequence 2, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-499-148-2
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Query Match
Best Local Similarity 10.0%; Score 104; DB 4; Length 162;
Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNOSQFCQIRIQGLAFYKHLLD--S 107
Db 27 EKNDCEKSKETLAENKLLPKMEEKDGCQSGF--NQAICLIKTAGLLEYQIYLDLQ 84
QY 108 DIFKGEALLPDSPEQLHTSLGLSOLLOPE-----DHPRETQOMPSSLSQQWQ 161
Db 85 NEYEGNQENVRD-----LRKNIRTLQILKOKIADLITTPATNTDLLEKMQSSNEW 139
QY 162 LRSKILRSLOAFIAAR 179
Db 140 KIILRLNLENFLOFSLR 157
```

```
RESULT 7
US-09-499-148-3
; Sequence 3, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
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; CURRENT APPLICATION NUMBER: US/09/499,148  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-499-148-3

Query Match 9.9%; Score 103; DB 4; Length 166;  
Best Local Similarity 24.8%; Pred. No. 0.00071;  
Matches 38; Conservative 28; Mismatches 55; Indels 32; Gaps 6;  
QY 52 GHMNLREEDEDE-----ETKNNVPRIQEDGDPQGLKDNSQFCQIRQGL 98  
DB 16 KGISALAKEMCDYNNKCEDSKAEALNNLPLKAEKDCGFCQSGF--NQETCLMRTITGL 73  
QY 99 AFYKHLDD--SDIFKGPALLPDSFMEQLHTSLGLSOLLQPEDHPRETQOMP-----149  
DB 74 QEFQIYLFQDKYEGD-----EENAKSVYVSTNVLQMLKRGKNQDEVITIPVPTVEVG 128  
QY 150 ---SLSSQWQRPRLRSKILRSLOAFIAAAR 179  
DB 129 LOAKLOSQEEWLRHTTHLTLRLLEDLFQFSLR 161

RESULT 8  
US-09-499-148-9  
; Sequence 9, Application US/09499148  
; Patent No. 6461604  
; GENERAL INFORMATION:  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.  
; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Sus scrofa domestica  
US-09-499-148-9

Query Match 9.6%; Score 100; DB 4; Length 166;  
Best Local Similarity 25.0%; Pred. No. 0.0015;  
Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps 5;  
QY 52 GHMNLREEDEDE-----ETKNNVPRIQEDGDPQGLKDNSQFCQIRQGL 98  
DB 16 KGISARKKCEKYEKCKENSKEVLAENNLPLKAEKDCGFCQSGF--NQETCLMRTITGL 73  
QY 99 AFYKHLDD--SDIFKGPALLPDSFMEQLHTSLGLSOLLQPEDHPRETQOMPES---150  
DB 74 VEFQIYLDYLOKEVESKNGN-----VEAVQISTKALITQLRQKGNPKDPKATTPNPTT 125  
QY 151 -----LSSSQWQRPRLRSKILRSLOAFIAAAR 179  
DB 126 NAGLLDKLQSONEMWKNKTKIILILRSLEDFLQFSLR 161

RESULT 9

US-09-499-148-7  
; Sequence 7, Application US/09499148  
; Patent No. 6461604  
; GENERAL INFORMATION:  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.  
; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-499-148-7

Query Match 9.2%; Score 96; DB 4; Length 166;  
Best Local Similarity 25.5%; Pred. No. 0.0044;  
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;  
QY 35 OLSRNLCLAWNNAHAPAGHMNLLREEDEETKNN--VPRIQEDGCDPQGLKDNSQFCQ 92  
DB 19 ENRKELC-----NGNSDC--MN-----NDALAEENLKLPEIQRNDGCVQTY--NQEICLL 66  
QY 93 RIRQGLAFYKHLDD-----SDIFKGPALLP-----DSPMEQLHTSL--GLSQ 134  
DB 67 KISSGLLEHVSHVLEYMKNNLKDKNKARVLQRDTETLIHIFNQEVKDLKHLVLTPTISN 126  
QY 135 LLOPEDHPRETQOMPESLSSQWQRPRLRSKILRSLOAFIAAAR 179  
DB 127 ALLTD-----KLESQKEWLRTKTIQFILKSLEEFKAVTLR 161

RESULT 10  
US-09-122-443-14  
; Sequence 14, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-14

Query Match          9.2%; Score 96; DB 3; Length 188;
Best Local Similarity 25.5%; Pred. No. 0.0052;
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGCDPQGLKDNSQFCLQ 92
Db 41 EMRKELC-----NGSDC--MN-----NDALAENNLKLPFIQRNDGCVQTYG--NQEICLL 88
QY 93 RIRQGLAFYKHLLD-----SDIFKGEPAALLP-----DSPMEQLHTSLL--GLSQ 134
Db 89 KISSGLLEVSHVLEYMKNNLKNKDKARVLQRTDTETLIHIFNQEVKDLHKIVLPTPISN 148
QY 135 LIQPEDHPRETQOMPSLSSSQOQRPLLRSKILRSLOAFLAIAAR 179
Db 149 ALLTD-----KLESQEWLRTKTIQFIKLSLEEFKVLTLR 183

RESULT 11
US-08-097-869-8
; Sequence 8, Application US/08097869
; Patent No. 6204364
; GENERAL INFORMATION:
; APPLICANT: Todaro, George J.
; APPLICANT: Rose, Timothy M.
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,869
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,178
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24455-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-097-869-8
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Query Match          9.2%; Score 96; DB 4; Length 211;
Best Local Similarity 25.5%; Pred. No. 0.0062;
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGCDPQGLKDNSQFCLQ 92
Db 64 EMRKELC-----NGSDC--MN-----NDALAENNLKLPFIQRNDGCVQTYG--NQEICLL 111
QY 93 RIRQGLAFYKHLLD-----SDIFKGEPAALLP-----DSPMEQLHTSLL--GLSQ 134
Db 112 KISSGLLEVSHVLEYMKNNLKNKDKARVLQRTDTETLIHIFNQEVKDLHKIVLPTPISN 171
QY 135 LIQPEDHPRETQOMPSLSSSQOQRPLLRSKILRSLOAFLAIAAR 179
Db 172 ALLTD-----KLESQEWLRTKTIQFIKLSLEEFKVLTLR 206

RESULT 12
US-08-209-182C-6
; Sequence 6, Application US/08209182C
; Patent No. 5545537
; GENERAL INFORMATION:
; APPLICANT: Skelly, Susan M.
; APPLICANT: Tackney, Charles T.
; APPLICANT: Snouwaert, John N.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/209,182C
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/724,698
; FILING DATE: 02-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: SKE-1-PD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-209-182C-6

Query Match          8.9%; Score 92.5; DB 1; Length 186;
Best Local Similarity 25.7%; Pred. No. 0.013;
Matches 36; Conservative 22; Mismatches 61; Indels 21; Gaps 4;

QY 53 HMNLLREEDEETKNNVPRIQCEGCDPQGLKDNSQFCLQRIQGLAFYKHLSDIFKQ 112
Db 50 NMSESSKEALAENNLNPKMAEKDCGQSGF--NETCLVKIITG-----LLEFEVYLE 101
QY 113 EPALLPDSPMEQ---LHTSLILGLSOLLQPE-----DHPRETQOMPSSSSQOQR 159
Db 102 IPPNRFESSEQARAVQMSTKVLQIFLOKAKNLDAITTPDPTTNASILLTQLQONWLQ 161
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QY 160 PLLRSKILRSLOAFIAAAR 179  
Db 162 DMTHILRSKFELQSSLR 181

RESULT 13  
PCT-US92-05612-6  
; Sequence 6, Application PC/TUS9205612  
; GENERAL INFORMATION:  
; APPLICANT: Skelly, Susan M.  
; APPLICANT: Tackney, Charles T.  
; APPLICANT: Snouwaert, John N.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ImClone Systems Incorporated  
; STREET: 180 Varick Street  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10014  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05612  
; FILING DATE: 19920702  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Felt, Irving N.  
; REGISTRATION NUMBER: 28,601  
; REFERENCE/DOCKET NUMBER: SKE-1-PT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-645-1405  
; TELEFAX: 212-645-2054  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 186 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-05612-6

Query Match 8.9%; Score 92.5; DB 5; Length 186;  
Best Local Similarity 25.7%; Pred. No. 0.013;  
Matches 36; Conservative 22; Mismatches 61; Indels 21; Gaps 4;

QY 53 HNNLLREDEETKNNVPRIQCDGCDPQGLKDNSQFCLORIQGLAFYKHLSDIFKG 112  
Db 50 NWSSESKALANNLNPKNMAEKDCGCSQGF--NEETCLVKIITG-----LLEFEVYLE 101

QY 113 EPALLPDSPMEO---LHTSLGLSLOLQPE-----DHPRETQOMPSLSSSQWQR 159  
Db 102 IPPNRFESSEQARAVOMSTKVLQFLQKKAKNLDAITTPDTTNASLLTKLQAOQNWLQ 161

QY 160 PLLRSKILRSLOAFIAAAR 179  
Db 162 DMTHILRSKFELQSSLR 181

RESULT 14  
US-09-499-148-6  
; Sequence 6, Application US/09499148  
; GENERAL INFORMATION:  
; PATENT NO. 6461604  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.

; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-499-148-6

Query Match 8.8%; Score 91; DB 4; Length 166;  
Best Local Similarity 24.5%; Pred. No. 0.016;  
Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;

QY 35 QLSRNLCLMAWNAHAPAGHMNLLREEDEETKNN--VPRIQCDGCDPQGLKDNSQFCLO 92  
Db 19 EMRKELC---NGNSDC--MN---SDDLSENMLKLEIQRNDGCFQGTGY--NQEICLL 66

QY 93 RIRQGLAFYKHLDD-----SDIFKGEPAALLPDSPMEOHLTSLGLSLOLQPEDH---PR 143  
Db 67 KICSGLEFEFYLEFVKNNLQDNKKDKARVIOSTETLVHI----FKOEIKDSYKIVLPT 122

QY 144 ETQQQ---MPSLSSSQWQRPLLRSKILRSLOAFIAAAR 179  
Db 123 PTSNALLMEKLESQKWLRTKTQILKALEFLKVTWR 161

RESULT 15  
US-09-487-792-14  
; Sequence 14, Application US/09487792  
; Patent No. 6433145  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Keratinocyte Derived Interferon  
; FILE REFERENCE: PF482Pl  
; CURRENT APPLICATION NUMBER: US/09/487,792  
; CURRENT FILING DATE: 2000-01-20  
; EARLIER APPLICATION NUMBER: 60/093,643  
; EARLIER FILING DATE: 1998-07-21  
; EARLIER APPLICATION NUMBER: PCT/US99/16424  
; EARLIER FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-487-792-14

Query Match 8.6%; Score 89; DB 4; Length 212;  
Best Local Similarity 22.0%; Pred. No. 0.038;  
Matches 39; Conservative 27; Mismatches 71; Indels 40; Gaps 7;

QY 15 WYTQGLAVPRSSSPDWAOQQQLSRNLCLMAWNAHAPAGHMNLLREEDEETKNNVPRIQC 74  
Db 59 YILDGISALRKET-----CNK--SNWCSSKEALA-----ENNINLPKXAK 97

QY 75 EDGCDPQGLKDNSQFCLORIQGLAFYKHLDD--SDIFKGEPAALLPDSPMEOHLTSLGL 132  
Db 98 EDGCFOSGF--NEETCLVKIITGLLEFEVYLEVLQNRFFS-----EQARAVOMSTKVL 150

QY 133 SLLQPE-----DHPRETQOMPSLSSSQWQRPLLRSKILRSLOAFIAAAR 179  
Db 151 IQFLQKKAKNLDAITTPDPTTNASLLTKLQAOQNWLQDMTHILRSKFELQSSLR 207

Search completed: November 20, 2002, 12:00:13

Job time : 13.2182 secs

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